

J807 Rec'd PCT/PTO 20 APR 2001

FORM PTO-1300 (REV 11-98)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEYS DOCKET NUMBER	
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371				VX012273 PCT	
INTERNATIONAL APPLICATION NO. PCT/JP99/05884		INTERNATIONAL FILING DATE 10/25/99		U.S. APPLICATION NO. (If known, see 37 CFR 1.5) 09/807933	
TITLE OF INVENTION ENDOGLUCANASES AND CELLULASE PREPARATIONS CONTAINING THE SAME				PRIORITY DATE CLAIMED 10/23/98	
APPLICANT(S) FOR DO/EO/US Yuko NAKAMURA et al.					
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:					
1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.					
2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.					
3. <input checked="" type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(l).					
4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.					
5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2))					
a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau).					
b. <input checked="" type="checkbox"/> has been transmitted by the International Bureau.					
c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US).					
6. <input checked="" type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371 (c)(2)).					
7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))					
a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau).					
b. <input type="checkbox"/> have been transmitted by the International Bureau.					
c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired.					
d. <input checked="" type="checkbox"/> have not been made and will not be made.					
8. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).					
9. <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)).					
10. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).					
Items 11. to 16. below concern document(s) or information included:					
11. <input checked="" type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98.					
12. <input checked="" type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.					
13. <input checked="" type="checkbox"/> A FIRST preliminary amendment.					
<input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.					
14. <input type="checkbox"/> A substitute specification.					
15. <input checked="" type="checkbox"/> A change of power of attorney and/or address letter.					
16. <input checked="" type="checkbox"/> Other items or information →					
(1) Nucleotide and/or Amino Acid Sequence Submission of: (a) Computer Readable Form (3 1/2 inch floppy disc), (b) Specification Sequence Listing on paper, and (c) Statement verifying identity of (a) and (b). (2) Submission of Deposit Receipts.					

U.S. APPLICATION NO. (if known 37 CFR 1.51) 09/807933		INTERNATIONAL APPLICATION NO. PCT/JP99/05884		ATTORNEYS DOCKET NUMBER VX012273 PCT	
17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)): <input type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$1,000.00 <input checked="" type="checkbox"/> International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$860.00 <input type="checkbox"/> International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$710.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$690.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) \$100.00				CALCULATIONS PTO USE ONLY	
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$	860.00
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	84 -20 =	64	X \$18.00	\$	1152.00
Independent claims	6 -3 =	3	X \$80.00	\$	240.00
<input type="checkbox"/> MULTIPLE DEPENDENT CLAIM(S) (if applicable)				+\$270.00	\$
TOTAL OF ABOVE CALCULATIONS =				\$	2252.00
<input type="checkbox"/> Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28).				\$	
SUBTOTAL =				\$	2252.00
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$	
TOTAL NATIONAL FEE =				\$	2252.00
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property				\$	40.00
TOTAL FEES ENCLOSED =				\$	2292.00
				Amount to be refunded	\$
				charged	\$

☐ Applicant claims small entity status. See 37 CFR 1.27.
☒ A check in the amount of \$ 2252.00 & 40.00 to cover the above fees is enclosed.
☐ Please charge my Deposit Account No. 22-0256 in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed.
☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 22-0256. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

DIRECT ALL CORRESPONDENCE TO:

VARNDELL & VARNDELL, PLLC
 106-A SOUTH COLUMBUS ST.
 ALEXANDRIA, VA 22314
 (703) 683-9730

Customer Number 021369

021369

PATENT TRADEMARK OFFICE

SIGNATURE
R. Eugene VarndeLL, Jr.
 NAME
29,728
 REGISTRATION NUMBER
4/20/01
 DATE

0000745 09/807933

JC08 Rec'd PCT/PTO 20 APR 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of:

Yuko NAKAMURA *et al.*

Serial No.: New

Based on PCT/JP99/05884

Filed: April 20, 2001 (herewith)

For: ENDOGLUCANASES AND CELLULASE
PREPARATIONS CONTAINING THE SAME

TRANSMITTAL OF SEQUENCE LISTING

Honorable Commissioner
of Patents and Trademarks
Washington, D.C. 20231

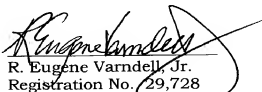
April 20, 2001

Dear Sir:

Please find attached hereto a paper copy of a Sequence Listing for the above-identified application that has been prepared in accordance with the sequence rules under 37 C.F.R. § 1.821 to 1.825. Also attached hereto is an envelope containing a copy of the Sequence Listing in computer readable form as required in 37 C.F.R. § 1.821(e).

In the event any additional fees are due, please charge our Deposit Account No. 22-0256.

Respectfully submitted,
VARNDELL & VARNDELL, PLLC
(formerly Varndell Legal Group)


R. Eugene Varndell, Jr.
Registration No. 29,728

Atty. Case No. VX012273 PCT
106-A South Columbus Street
Alexandria, Virginia 22314
(703) 683-9730

\\V2\DOCS\W_DOCS\APR01\PO80-2273 PCT SL.DOC

09/807933

JCOS Rec'd PCT/PTO 20 APR 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of:

Yuko NAKAMURA *et al.*

Serial No.: New

Based on PCT/JP99/05884

Filed: April 20, 2001 (herewith)

For: ENDOGLUCANASES AND CELLULASE
PREPARATIONS CONTAINING THE SAME

PRELIMINARY AMENDMENT

Honorable Commissioner
of Patents and Trademarks
Washington, D.C. 20231

April 20, 2001

Dear Sir:

Prior to an examination under merits, please amend the above-identified application as follows:

IN THE CLAIMS:

Please cancel claim 57 without prejudice or disclaimer of the subject matter set forth therein. Please amend claims 4, 6, 8, 13, 14, 16, 18-23, 26, 28, 32, 34-36, 41, 55, 56, 60, 62, 64, 71, 73-85 to read as follows:

--4. (Amended) The enzyme according to claim 1, wherein the enzyme is derived from the genus *Rhizopus* and has an average molecular weight of approximately 40 kD as determined by SDS-PAGE.--

--6. (Amended) The enzyme according to claim 1, wherein the enzyme is derived from the genus *Mucor* and has an average molecular weight of approximately 41 kD as determined by SDS-PAGE.--

--8. (Amended) The enzyme according to claim 1, wherein the enzyme is derived from the genus *Phycomyces* and has an average molecular weight of approximately 45 kD as determined by SDS-PAGE.--

--13. (Amended) The enzyme according to claim 10, wherein the cellulose binding domain consists of the following amino acid sequence (III):
Cys-Ser-X1-X2-Tyr-X3-Gln-Cys-Gly-Gly-X4-X5-Trp-X6-Gly-Pro-Thr-Cys-Cys-X7-X8-Gly-X9-Thr-Cys-X10-X11-X12-X13-X14-Asn-X15-X16-Tyr-Ser-Gln-Cys-X17 (III) (SEQ ID NO: 20)

wherein:

X1 is Lys, Ser or Gln;

X2 is Leu, Ala, Val or Gly;

X3 is Gly, Tyr or Ser;

X4 is Lys or Ile;

X5 is Asn, Asp, Gly or Met;

X6 is Asn, Asp, Ser or Thr;

X7 is Glu, Asp or Thr;

X8 is Ser or Ala;

X9 is Ser or Phe;

X10 is Lys or Val;

X11 is Val, Asp, Ala or Gly;

X12 is Ser, Tyr, Gln or Ala;

X13 is Pro, Glu or Lys, or is absent;

X14 is Asp, Gly or Asn, or is absent;

X15 is Asp, Pro, Lys or Glu;

X16 is Tyr, Phe or Trp;

X17 is Leu, Val or Ile; and

one of X4 or X15 is Lys and the other is any amino acid residue except Lys.--

14. (Amended) The enzyme according to claim 10, wherein the cellulose binding domain consists of the following amino acid sequence (IV):
Cys-Ser-Lys-X21-Tyr-X22-Gln-Cys-Gly-Gly-Lys-X23-Trp-X24-Gly-Pro-Thr-Cys-Cys-
Glu-Ser-Gly-Ser-Thr-Cys-X25-X26-X27-X28-X29-Asn-X30-X31-Tyr-Ser-Gln-Cys-X32
(IV) (SEQ ID NO: 21)

wherein:

X21 is Leu or Ala;

X22 is Gly or Tyr;

X23 is Asn or Asp;

X24 is Asn or Asp;

X25 is Lys or Val;

X26 is Val or Asp;

X27 is Ser or Tyr;

X28 is Pro, or is absent;

X29 is Asp, or is absent;

X30 is Asp or Pro;

X31 is Tyr or Phe; and

X32 is Leu or Val.--

--16. (Amended) The enzyme according to claim 10, wherein the cellulose binding domain consists of the following amino acid sequence (V):

Cys-Ser-Ser-Val-Tyr-X41-Gln-Cys-Gly-Gly-Ile-Gly-Trp-X42-Gly-Pro-Thr-Cys-Cys-X43-X44-Gly-Ser-Thr-Cys-X45-Ala-Gln-X46-X47-Asn-Lys-Tyr-Tyr-Ser-Gln-Cys-X48 (V)
(SEQ ID NO: 25)

wherein:

X41 is Gly or Ser;

X42 is Ser or Thr;

X43 is Glu or Asp;

X44 is Ser or Ala;

X45 is Val or Lys;

X46 is Glu or Lys;

X47 is Gly or Asp; and

X48 is Leu or Ile.--

--18. (Amended) The enzyme according to claim 10, wherein the cellulose binding domain consists of the amino acid sequence of SEQ ID NO: 28.

19. (Amended) The enzyme according to claim 10, wherein the cellulose binding domain is located on its N-terminal side.

20. (Amended) The enzyme according to claim 10, wherein the enzyme is capable of removing fuzz completely from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.

21. (Amended) The enzyme according to claim 10, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

22. (Amended) The enzyme according to claim 10, wherein the enzyme is derived from *Zygomycotina*.

23. (Amended) The enzyme according to claim 10, wherein the enzyme further comprises a part of its linker region consisting of the following amino acid sequence (VI):

Tyr-Xaa-Xaa-Xaa-X51-Gly-Gly-Xaa-X52-Gly (VI) (SEQ ID NO: 31)

wherein Xaa is independently any amino acid residue; and X51 and X52 are independently Ser or Thr.--

--26. (Amended) The enzyme according to claim 23, wherein both X51 and X52 are Ser.--

--28. (Amended) The enzyme according to claim 23, wherein the part of the linker region is located on the N-terminal side of the catalytic domain.--

--32. (Amended) The enzyme according to claim 29, wherein both X51 and X52 are Ser.--

--34. (Amended) The enzyme according to claim 29, wherein the enzyme is capable of removing fuzz completely from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.

35. (Amended) The enzyme according to claim 29, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

36. (Amended) The enzyme according to claim 29, wherein the enzyme is derived from *Zygomycotina*.--

--38. (Amended) The enzyme according to claim 37, wherein the cellulose-binding domain consists of the amino acid sequence described in claim 10.--

--41. (Amended) The enzyme according to claim 1, wherein the enzyme or the modified protein is modified so that Asn-linked oligosaccharide chains are not added thereto.--

--55. (Amended) The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that the cellulose binding domain represents the amino acid sequence (I) described in claim 10, and which may have a modification(s) in a region(s) other than said cellulose binding domain.

56. (Amended) The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that a part of the linker region represents the amino acid sequence (VI) or (VII) described in claim 23 and which may have a modification(s) in a region(s) other than said part of the linker region.--

--60. (Amended) A polynucleotide comprising a nucleotide sequence encoding the enzyme, protein, modified protein or homologue according to claim 1.--

--62. (Amended) The polynucleotide according to claim 60, wherein said polynucleotide comprises a nucleotide sequence in which codons have been optimized for a host by selecting those codons frequently used by the host.--

--64. (Amended) An expression vector comprising the polynucleotide according to claim 60.

65. (Amended) A host cell transformed with the polynucleotide according to claim 60.--

--71. (Amended) A method for producing the enzyme, protein, modified protein or homologue, comprising cultivating the host cell according to claim 63 and recovering the enzyme, protein, modified protein or homologue from said host cell and/or the resultant cultivation broth.--

--73. (Amended) A cellulase preparation comprising the enzyme, protein, modified protein or homologue according to claim 1.

74. (Amended) A method of treating cellulose-containing fabrics, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1.

75. (Amended) A method of reducing the rate at which cellulose-containing fabrics become fuzzy or for reducing fuzzing in cellulose-containing fabrics, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1.

76. (Amended) A method of weight loss treatment for cellulose-containing fabrics to improve its touch and appearance, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1.

77. (Amended) A method of providing color clarification of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1.

78. (Amended) A method of providing a localized variation in color of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1.

79. (Amended) A method of reducing the rate at which cellulose-containing fabrics become stiff or reducing stiffness in cellulose-containing fabrics, comprising a step of treating the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1.

80. (Amended) The method according to claim 74, wherein the treatment of the fabrics is performed through soaking, washing or rinsing the fabrics.

81. (Amended) An additive to detergent comprising the enzyme, protein, modified protein or homologue according to claim 1 in a non-scattering granular form or a stabilized liquid form.

82. (Amended) A detergent composition comprising the enzyme, protein, modified protein or homologue according to claim 1.

83. (Amended) A method of improving the freeness of a paper pulp, comprising a step of treating the paper pulp with the enzyme, protein, modified protein or homologue according to claim 1.

84. (Amended) A method of deinking a waste paper, comprising a step of treating the waste paper with the endoglucanase, modified protein or homologue according to claim 1 in the presence of a deinking agent.

85. (Amended) A method of improving the digestibility of an animal feed, comprising a step of treating a cellulose-containing feed with the enzyme, protein, modified protein or homologue according to claim 1.--

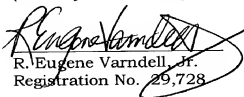
REMARKS

In the foregoing amendments, applicant's claims were amended to remove multiple dependent claims. Claim 57 was cancelled. Early consideration and allowance of claims 1-56 and 58-85 are respectfully requested.

Attached hereto is a marked-up version of the changes made to the claims. The attached pages are captioned "**Version with markings to show changes made.**" Early consideration and allowance of claims 1-56 and 58-85 are respectfully requested.

In the event any additional fees are due, please charge our Deposit Account No. 22-0256.

Respectfully submitted,
VARNDELL & VARNDELL, PLLC
(formerly Varndell Legal Group)


R. Eugene Varndell, Jr.
Registration No. 29,728

Atty. Case No. VX012273 PCT
106-A South Columbus Street
Alexandria, Virginia 22314
(703) 683-9730
\\V2\DOCS\W_DOCS\APR01\PO80-2273 PCT PA.DOC

New US National Phase Application Based on PCT/JP99/05884

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS:

Claims 4, 6, 8, 13, 14, 16, 18-23, 26, 28, 32, 34-36, 41, 55, 56, 60, 62, 64, 71, 73-85 were amended as follows:

--4. (Amended) The enzyme according to claim 1 ~~any one of claims 1 to 3~~, wherein the enzyme is derived from the genus *Rhizopus* and has an average molecular weight of approximately 40 kD as determined by SDS-PAGE.--

--6. (Amended) The enzyme according to claim 1 ~~any one of claims 1 to 3~~, wherein the enzyme is derived from the genus *Mucor* and has an average molecular weight of approximately 41 kD as determined by SDS-PAGE.--

--8. (Amended) The enzyme according to claim 1 ~~any one of claims 1 to 3~~, wherein the enzyme is derived from the genus *Phycomyces* and has an average molecular weight of approximately 45 kD as determined by SDS-PAGE.--

--13. (Amended) The enzyme according to claim 10 ~~or 11~~, wherein the cellulose binding domain consists of the following amino acid sequence (III):

Cys-Ser-X1-X2-Tyr-X3-Gln-Cys-Gly-Gly-X4-X5-Trp-X6-Gly-Pro-Thr-Cys-Cys-X7-X8-Gly-X9-Thr-Cys-X10-X11-X12-X13-X14-Asn-X15-X16-Tyr-Ser-Gln-Cys-X17 (III) (SEQ

ID NO: 20)

wherein:

X1 is Lys, Ser or Gln;

X2 is Leu, Ala, Val or Gly;

X3 is Gly, Tyr or Ser;

X4 is Lys or Ile;

X5 is Asn, Asp, Gly or Met;

X6 is Asn, Asp, Ser or Thr;

X7 is Glu, Asp or Thr;

X8 is Ser or Ala;

X9 is Ser or Phe;

X10 is Lys or Val;

X11 is Val, Asp, Ala or Gly;

X12 is Ser, Tyr, Gln or Ala;

X13 is Pro, Glu or Lys, or is absent;

X14 is Asp, Gly or Asn, or is absent;

X15 is Asp, Pro, Lys or Glu;

X16 is Tyr, Phe or Trp;

X17 is Leu, Val or Ile; and

one of X4 or X15 is Lys and the other is any amino acid residue except Lys.--

14. (Amended) The enzyme according to claim 10 ~~or 11~~, wherein the cellulose binding domain consists of the following amino acid sequence (IV):
Cys-Ser-Lys-X21-Tyr-X22-Gln-Cys-Gly-Gly-Lys-X23-Trp-X24-Gly-Pro-Thr-Cys-Cys-
Glu-Ser-Gly-Ser-Thr-Cys-X25-X26-X27-X28-X29-Asn-X30-X31-Tyr-Ser-Gln-Cys-X32
(IV) (SEQ ID NO: 21)

wherein:

X21 is Leu or Ala;

X22 is Gly or Tyr;

X23 is Asn or Asp;
X24 is Asn or Asp;
X25 is Lys or Val;
X26 is Val or Asp;
X27 is Ser or Tyr;
X28 is Pro, or is absent;
X29 is Asp, or is absent;
X30 is Asp or Pro;
X31 is Tyr or Phe; and
X32 is Leu or Val.--

--16. (Amended) The enzyme according to claim 10 ~~or 11~~, wherein the cellulose binding domain consists of the following amino acid sequence (V):

Cys-Ser-Ser-Val-Tyr-X41-Gln-Cys-Gly-Gly-Ile-Gly-Trp-X42-Gly-Pro-Thr-Cys-Cys-X43-
X44-Gly-Ser-Thr-Cys-X45-Ala-Gln-X46-X47-Asn-Lys-Tyr-Tyr-Ser-Gln-Cys-X48 (V)
(SEQ ID NO: 25)

wherein:

X41 is Gly or Ser;
X42 is Ser or Thr;
X43 is Glu or Asp;
X44 is Ser or Ala;
X45 is Val or Lys;
X46 is Glu or Lys;
X47 is Gly or Asp; and
X48 is Leu or Ile.--

--18. (Amended) The enzyme according to claim 10 ~~or 11~~, wherein the cellulose binding domain consists of the amino acid sequence of SEQ ID NO: 28.

19. (Amended) The enzyme according to claim 10 ~~or 11~~, wherein the cellulose binding domain is located on its N-terminal side.

20. (Amended) The enzyme according to claim 10 ~~any one of claims 10 to 19~~, wherein the enzyme is capable of removing fuzz completely from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.

21. (Amended) The enzyme according to claim 10 ~~any one of claims 10 to 20~~, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

22. (Amended) The enzyme according to claim 10 ~~any one of claims 10 to 21~~, wherein the enzyme is derived from *Zygomycotina*.

23. (Amended) The enzyme according to claim 10 ~~any one of claims 10 to 22~~, wherein the enzyme further comprises a part of its linker region consisting of the following amino acid sequence (VI):
Tyr-Xaa-Xaa-Xaa-X51-Gly-Gly-Xaa-X52-Gly (VI) (SEQ ID NO: 31)
wherein Xaa is independently any amino acid residue; and X51 and X52 are independently Ser or Thr.--

--26. (Amended) The enzyme according to claim 23 ~~any one of claims 23 to 25~~, wherein both X51 and X52 are Ser.--

--28. (Amended) The enzyme according to claim 23 ~~any one of claims 23 to 27~~, wherein the part of the linker region is located on the N-terminal side of the catalytic domain.--

--32. (Amended) The enzyme according to claim 29 ~~any one of claims 29 to 31~~, wherein both X51 and X52 are Ser.--

--34. (Amended) The enzyme according to claim 29 ~~any one of claims 23 to 33~~, wherein the enzyme is capable of removing fuzz completely from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.

35. (Amended) The enzyme according to claim 29 ~~any one of claims 23 to 34~~, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

36. (Amended) The enzyme according to claim 29 ~~any one of claims 23 to 35~~, wherein the enzyme is derived from *Zygomycotina*.--

--38. (Amended) The enzyme according to claim 37, wherein the cellulose-binding domain consists of the amino acid sequence described in claim 10 ~~any one of claims 10 to 18~~.--

--41. (Amended) The enzyme according to claim 1 ~~any one of claims 1 to 39 or the modified protein according to claim 40~~, wherein the enzyme or the modified protein is modified so that Asn-linked oligosaccharide chains are not added thereto.--

--55. (Amended) The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that the cellulose binding domain represents ~~one of~~ the amino acid sequences (I) to (V) described in claims 10, ~~11, 13, 14 and 16, respectively~~, and which may have a modification(s) in a region(s) other than said cellulose binding domain.

56. (Amended) The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that a part of the linker region represents the amino acid sequence (VI) or (VII) described in claim 23 ~~or 24~~ and which may have a modification(s) in a region(s) other than said part of the linker region.--

--60. (Amended) A polynucleotide comprising a nucleotide sequence encoding the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59~~--

--62. (Amended) The polynucleotide according to claim 60 ~~or 61~~, wherein said polynucleotide comprises a nucleotide sequence in which codons have been optimized for a host by selecting those codons frequently used by the host.--

--64. (Amended) An expression vector comprising the polynucleotide according to claim 60 ~~any one of claims 60 to 63~~.

65. (Amended) A host cell transformed with the polynucleotide according to claim 60 ~~any one of claims 60 to 63 or the expression vector according to claim 64.~~

--71. (Amended) A method for producing the enzyme, protein, modified protein or homologue ~~according to any one of claims 1 to 59~~, comprising cultivating the host cell according to claim 63 ~~any one of claims 63 to 70~~ and recovering the enzyme, protein, modified protein or homologue from said host cell and/or the resultant cultivation broth.--

--73. (Amended) A cellulase preparation comprising the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72.~~

74. (Amended) A method of treating cellulose-containing fabrics, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.~~

75. (Amended) A method of reducing the rate at which cellulose-containing fabrics become fuzzy or for reducing fuzzing in cellulose-containing fabrics, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.~~

76. (Amended) A method of weight loss treatment for cellulose-containing fabrics to improve its touch and appearance, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue

according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.~~

77. (Amended) A method of providing color clarification of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.~~

78. (Amended) A method of providing a localized variation in color of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.~~

79. (Amended) A method of reducing the rate at which cellulose-containing fabrics become stiff or reducing stiffness in cellulose-containing fabrics, comprising a step of treating the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.~~

80. (Amended) The method according to claim 74 ~~any one of claims 74 to 79~~, wherein the treatment of the fabrics is performed through soaking, washing or rinsing the fabrics.

81. (Amended) An additive to detergent comprising the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73~~ in a non-scattering granular form or a stabilized liquid form.

82. (Amended) A detergent composition comprising the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73~~.

83. (Amended) A method of improving the freeness of a paper pulp, comprising a step of treating the paper pulp with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73~~.

84. (Amended) A method of deinking a waste paper, comprising a step of treating the waste paper with the endoglucanase, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73~~ in the presence of a deinking agent.

85. (Amended) A method of improving the digestibility of an animal feed, comprising a step of treating a cellulose-containing feed with the enzyme, protein, modified protein or homologue according to claim 1 ~~any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73~~.

3/PRTS

09/807933

JC08 Rec'd PGT/PTO 20 APR 2001

ENDOGLUCANASES AND CELLULASE PREPARATIONS CONTAINING THE SAME

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates to endoglucanases and cellulase preparations containing the same, as well as methods of treating cellulose-containing fabrics, papers, pulps or animal feeds with the cellulase preparations.

Background Art

Treatment of cellulose-containing fabrics with cellulase is carried out to give the fabrics desired properties. For example, treatment with cellulase is carried out in the fiber industry in order to improve the touch and appearance of cellulose-containing fabrics or to give colored cellulose-containing fabrics an appearance of "stone-washed" material, i.e. partial color change (European Patent No. 307,564).

On the other hand, lyocell which is a regenerated cellulose fiber prepared from wood pulp-derived cellulose by an organic solvent spinning process has been attracting attention recently for its properties (such as high strength, water absorption) and the production process that causes less environmental pollution. However, since lyocell generates fuzz during its production, lyocell in that form is commercially evaluated rather low as a fabric product. Then, methods of removing the fuzz generating during production using cellulase have been proposed.

The term "cellulose-containing fabrics" used herein include fabrics prepared from cellulosic fiber materials such as natural cellulose (e.g., cotton, linen), regenerated cellulose (e.g., lyocell, rayon, polynosic, cupraammonium rayon); woven or knitted cloths from these fibers; and clothing items prepared by sewing these cloths. Further, those fabrics, cloths and sewn clothing items which comprise cellulosic fiber material(s) and other material(s) such as synthetic fiber, wool or silk, are also included in this term.

At present, cellulases derived from *Trichoderma* and *Humicola* (both are wood-rotting fungi) are mainly used in the treatment of cellulose-containing fabrics. These cellulases are mixtures of a plurality of cellulase components. Practical use of these cellulases has been hindered by the difficulty that a large quantity of cellulase preparation is

needed in order to achieve a desired effect on a cellulose-containing fabrics.

The above-described drawback of these cellulose preparations is being improved by the development of preparations containing a large quantity of endoglucanases. For example, a number of endoglucanase-enriched cellulase preparations are disclosed in WO89/09259, WO91/17243, WO98/03640 and WO94/21801. In particular, WO91/17243 discloses that a *Humicola*-derived purified 43 kD endoglucanase component (EGV) exhibits jeans decoloring activity about 100-fold greater than that activity of conventional cellulase preparations which are mixtures of a plurality of cellulase components. WO98/03640 discloses that a *Humicola*-derived endoglucanase component NCE4 exhibits jeans decoloring activity and lyocell fuzz removal activity which are 25-fold and 100-fold greater than those activities of the conventional cellulase preparations, respectively. However, in order to remove strong fuzz generated in regenerated cellulose fabrics such as lyocell, cellulase preparations containing endoglucanase components of still higher activity are required to put them into practical use on an industrial scale.

Generally, the processing of cellulose-containing fabrics includes refining, bleaching, dyeing and mercerization; all of them are carried out under alkaline conditions. However, in the above-described conventional cellulose preparations containing a large quantity of endoglucanase, those derived from *Trichoderma* have an optimum pH in an acidic range and those derived from *Humicola* have an optimum pH in a neutral range. Thus, when these cellulase preparations are used, the cellulase treatment should be carried out separately from the above-mentioned fabrics processing steps, after pH adjustment by addition of buffers, etc.

Accordingly, if an endoglucanase component functioning under alkaline conditions is available, cellulase treatment can be carried out in the above-mentioned fabric processing steps. Thus, production steps can be shortened. As a result, it is believed that a great cost reduction can be achieved.

It is disclosed that *Rhizopus*-derived cellulases are capable of retaining their activity under alkaline conditions (Japanese Unexamined Patent Publications Nos. 60-226599, 64-40667, 64-26779 and 7-90300). In all of these disclosures, *Rhizopus* cultivation preparations are used for the purpose of providing detergents for use in the washing/rinsing

of clothing. However, the activity of these *Rhizopus* cultivation preparations is extremely low and by far below the level required for practical use.

Highly active cellulase preparations are often provided as preparations containing a large quantity of endoglucanase as described above. For preparing such endoglucanase, methods are known in which an endoglucanase component of interest is recombinantly expressed in a host cell in a large quantity as described in WO91/17243, WO98/03667 and WO98/111239. Examples of preferable host cells in these methods include filamentous fungi belonging to *Deuteromycotina*, e.g., *Aspergillus*, *Humicola*, and *Trichoderma*. Considering enzyme production at an industrial level, these filamentous fungi belonging to *Deuteromycotina* will be extremely excellent hosts.

However, when a heterogeneous gene is expressed in these filamentous fungi belonging to *Deuteromycotina*, high expression is often hindered for reasons such as difference in codon usage. In particular, there has been no report of high expression of a gene derived from the genus *Rhizopus* belonging to *Zygomycotina* in the above-mentioned filamentous fungi belonging to *Deuteromycotina*. Thus, technology for high expression has been desired.

Under such circumstances, recently, a technology is being constructed which achieves high expression of a gene of interest in a host cell by optimizing the codons of the gene in conformity with the codon frequency in the host cell. The optimum use of codons for high expression of a gene of interest in a host may be presumed by examining the codon frequency in those genes expressed relatively abundantly in the host in natural environment. This is supported by the report of Lloyd et al. (Andrew T. Lloyd and Paul M. Sharp, 1991, Mol. Gen. Genet. 230, 288-294) concerning the codon frequency in *Aspergillus nidulans*, a filamentous fungus belonging to *Deuteromycotina*. However, even if information on appropriate codon use has been obtained from known DNA sequences, that information does not necessarily result in the realization of high expression of a gene of interest immediately. Especially, in filamentous fungi, which are complex to control, selection of a single sequence most suitable for expression from a number of sequences having suitable codon use has been required.

SUMMARY OF THE INVENTION

The present inventors have isolated highly active endoglucanases and genes thereof from *Zygomycotina* fungi *Rhizopus oryzae*, *Mucor circinelloides* and *Phycomyces nitens*. The inventors have found that these enzymes exhibit extremely strong activities in the removal of fuzz from regenerated cellulose fabrics and that they retain very strong activities under alkaline conditions. These endoglucanases have remarkably high activities 10- to 20-fold higher in neutral range and 20- to 50-fold higher in alkaline range than the activities of EGV (WO91/17243) and NCE4 (WO98/03640) derived from *Humicola* which are known to have high activities in fuzz removal from cellulose-containing fabrics.

Furthermore, even when these endoglucanases are used in a form of detergent composition for use at low temperatures and under alkaline conditions in general, it has been found that they have strong activities in the removal of fuzz from cotton. For example, these highly active endoglucanases have strong activities 2- to 20-fold greater than the activities of *Humicola*- derived EGV (WO91/17243) and NCE4 (WO98/03640) which are known to have strong activities in the removal of fuzz when used as a detergent.

More surprisingly, the present inventors have found that these endoglucanases have completely novel and characteristic amino acid sequences. Briefly, the conserved consensus sequence Gln-Cys-Gly-Gly in their cellulose binding domains is followed by Lys; or the conserved consensus residue Asn in the domain is followed by Lys.

Further, the present inventors have found a completely novel and characteristic sequence that is believed to be necessary for removal of fuzz from regenerated cellulose fabrics, in a part of their linker domains located close to the N-terminus of their catalytic domains.

Further, the present inventors have also found that these endoglucanases have a structure completely new as filamentous fungi-derived endoglucanases belonging to family 45 in the sense that their cellulose binding domains are located on the N-terminal side.

It is an object of the invention to provide enzymes, which exhibit very high endoglucanase activity on regenerated cellulose and retain high activity under alkaline conditions; and genes encoding the enzymes.

It is another object of the invention is to provide cellulase preparations with good properties.

It is still another object of the invention to provide effective and inexpensive methods of treating cellulose-containing fabrics, papers, pulps and animal feeds with the above-described enzymes.

The enzyme according to the present invention has the following properties:

- a) exhibiting endoglucanase activity; and
- b) capable of completely removing fuzz from a regenerated cellulose fabric at a concentration of 1 mg of the protein/L or below.

In another aspect of the invention, the enzyme having endoglucanase activity is a protein comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11; a modified protein thereof exhibiting endoglucanase activity; or a homologue of the protein or the modified protein.

Further, the gene of the invention for the enzyme having endoglucanase activity comprises a nucleotide sequence encoding the above enzyme (e.g., the nucleotide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12 or 13).

Further, the cellulase preparation of the invention comprises the above-described enzyme exhibiting endoglucanase activity.

Further, the method of the invention for treating cellulose-containing fabrics or the like comprises contacting the cellulose-containing fabrics or the like with the enzyme of the invention exhibiting endoglucanase activity or the cellulase preparation of the invention.

BRIEF DESCRIPTION OF THE INVENTION

Fig. 1 is a graph showing the relationship between reaction pH and relative activity in the removal of fuzz from lyocell on endoglucanases RCE I, MCE I, PCE I and NCE4.

Fig. 2 is a graph showing the relationship between reaction pH and relative activity in the removal of fuzz from lyocell on mutant endoglucanases RCE I, MCE I and endoglucanase NCE4.

Fig. 3 is a table showing the codon frequency in the gene encoding RCE I.

Fig. 4 is a table showing the codon frequency in the gene encoding NCE 1.

Fig. 5 is a table showing the codon frequency in the gene encoding NCE 2.

Fig. 6 is a table showing the codon frequency in the gene encoding NCE 4.

DISCLOSURE OF THE INVENTION

Definition

Amino acids are expressed in three-letter abbreviations.

The term "any amino acid residue" used herein includes Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

The term "nucleotide sequence" used herein includes not only DNA sequences but also RNA sequences.

Deposit of Microorganisms

Rhizopus oryzae CP96001 strain was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology (1-3 Higashi 1-chome, Tsukuba City, Ibaraki Pref., Japan) under the accession No. FERM BP-6889 on April 21, 1997.

Mucor circinelloides CP99001 strain was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology under the accession No. FERM BP-6890 on July 2, 1999.

Phycomyces nitens CP99002 strain was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology under the accession No. FERM BP-6891 on July 2, 1999.

Enzymes exhibiting endoglucanase Activity

The enzyme of the invention has higher activity than hitherto known highly active endoglucanases in the removal of fuzz from regenerated cellulose fabrics such as lyocell, and has an advantage that it functions even under alkaline conditions. The high activity of the enzyme of the invention enables practical use of the enzyme because only a small

quantity of cellulase preparation containing the enzyme is required to give desired effects on regenerated cellulose fabrics. Furthermore, the advantage that the enzyme functions even under alkaline conditions enables fuzz removal processing of regenerated cellulose fabrics under alkaline conditions which is now believed impossible. Thus, according to the enzyme of the invention, fabric-processing steps can be shortened and cost reduction can be realized.

Lyocell is a term for a regenerated cellulose fabric designated formerly by the Comite International de la Rayonne et des Fibres Synthetiques (CIRFS). As a common product, it is called Tencel™ (a trademark of Acordis Fibers). Since lyocell is a fiber prepared from wood pulp-derived cellulose by an organic solvent spinning process, it is classified into regenerated cellulose fiber. The other regenerated cellulose fibers such as viscose, rayon and polynosic are also prepared from wood pulp-derived cellulose and have the same crystal structure as that of lyocell. Therefore, when applied to these regenerated cellulose fibers, the enzyme according to the invention is capable of producing effects similar to those produced when applied to lyocell.

According to the first aspect of the invention, enzymes having the above-described properties a) and b) are provided.

Details of the properties of the enzyme according to the invention are as described blow.

(i) **Function and Substrate Specificity**

The enzyme of the invention is an enzyme exhibiting endoglucanase activity, i.e. endo-1,4- β -glucanase EC3.2.1.4. Specifically, the enzyme of the invention hydrolyzes the β -1,4-glucopyranosyl bond of β -1,4-glucan. This enzyme specifically acts on a regenerated cellulose fabric such as lyocell as a substrate, and is capable of removing fuzz from Tencel™ completely at an extremely low concentration (0.2-1.0 mg of the protein/L).

The term "activity of fuzz removal from a regenerated cellulose fabric" used herein means the activity that is evaluated by the method described in Example A4 or A5.

The expression "capable of completely removing fuzz from a regenerated cellulose fabric" used herein refers to a state in which no fuzz can be detected by the eye when a knit lyocell cloth that has been dyed brown and undergone fuzz-raising treatment is treated with

an enzyme for fuzz removal. Specifically, the expression refers to a state of the fuzz-removed cloth in which the L* value (lightness) of L*a*b* color system as determined with a spectrophotometer (Minolta; model CM525i) under the conditions described in Example A6 is 24.5 or less. The cloth dyed brown before fuzz-raising treatment refers to a cloth whose L* value is in the range from 24 to 26; a* value (chromaticity) is in the range from 4.7 to 5.1; and b* value is in the range from 7.2 to 7.9. This lyocell cloth is a knit smooth cloth prepared with No. 40/1 count yarn and with gauge 30" *24G and then dyed brown with Sumifix (Sumitomo Chemical). As a specific example of a knit lyocell cloth product, OT7440 Knit Smooth (Toshima Co., Ltd.) may be given. In the above-mentioned fuzz-raising treatment, fuzz should be generated until the L* value reaches approximately 30 when a cloth with this color (brown) is used.

(ii) Optimum pH and pH at which the Enzyme is Stable

The fuzz removal activity of the endoglucanase of the invention when it is acted on regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

The *Rhizopus oryzae*-derived endoglucanase has high CMCase activity at pH 4-8, though the optimum pH for this activity is about 5. Also, it has high lyocell fuzz removal activity at pH 5-9, though the optimum pH for this activity is about 5.

The *Mucor circinelloides*-derived endoglucanase has high CMCase activity at pH 5-8, though the optimum pH for this activity is about 6. Also, it has high lyocell fuzz removal activity at pH 5-9, though the optimum pH for this activity is 5-6.

The *Phycomyces nitens*-derived endoglucanase has high CMCase activity at pH 5-8, though the optimum pH for this activity is about 6. Also, it has high lyocell fuzz removal activity at pH 5-8, though the optimum pH for this activity is about 6.

(iii) Optimum Temperature and Thermal Stability

The *Rhizopus oryzae*-derived endoglucanase has high CMCase activity at 45-65°C, though the optimum temperature range for this activity is 55-60°C. Also, it has high lyocell fuzz removal activity at 45-60°C, though the optimum temperature for this activity is about 55°C.

The *Mucor circinelloides*-derived endoglucanase has high CMCase activity at

40-60°C, though the optimum temperature range for this activity is 45-55°C. Also, it has high lyocell fuzz removal activity at about 45-55°C, though the optimum temperature for this activity is about 50°C.

The *Phycomyces nitens*-derived endoglucanase has high CMCase activity at about 40-60°C, though the optimum temperature range for this activity is 45-55°C. Also, it has high lyocell fuzz removal activity at about 45-55°C, though the optimum temperature for this activity is about 50°C.

(iv) Molecular Weight

The *Rhizopus oryzae*-derived endoglucanase may have a molecular weight of approximately 40 kDa; the *Mucor circinelloides*-derived endoglucanases may have a molecular weight of approximately 41 kDa; and the *Phycomyces nitens*-derived endoglucanase may have a molecular weight of approximately 45 kDa as determined by SDS-PAGE.

(v) N-Terminal Sequence

The *Rhizopus oryzae*-derived endoglucanase may have an N-terminal sequence represented by the amino acid sequence of SEQ ID NO: 14. The *Mucor circinelloides*-derived endoglucanase may have an N-terminal sequence represented by the amino acid sequence of SEQ ID NO: 15. The *Phycomyces nitens*-derived endoglucanase may have an N-terminal sequence represented by the amino acid sequence of SEQ ID NO: 16.

(vi) Cellulose Binding Domain

It is known that cellulases generally have a cellulose binding domain (CBD) at which they bind to cellulose. Further, it has been confirmed that filamentous fungi-derived cellulose binding domains have the following consensus sequence conserved (Hoffren, A.-M. et al, Protein Engineering 8:443-450, 1995):

```

Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa
1                                     10
Gly Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
20
Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Gln Cys Xaa (SEQ ID NO: 17)

```

30

wherein Xaa is independently any amino acid; and Xaa's at positions 20, 21, 22, 23, 24, 30 and 31 may be independently absent.

In the above sequence, the conserved consensus sequence Gln-Cys-Gly-Gly is usually followed by Ile, Gln, Ala, Ser or Asn; this consensus sequence followed by Lys has not been found. Also, the conserved consensus residue Asn in the above-described sequence is usually followed by Asp, Pro, Gln, Tyr or Ala; this consensus residue followed by Lys has not been found. The present inventors have found that the consensus sequence Gln-Cys-Gly-Gly is followed by Lys in the cellulose binding domains of RCE I, RCE II, RCE III and PCE I, and that the consensus residue Asn is followed by Lys in the cellulose binding domains of MCE I and MCE II. These are completely novel amino acid sequences.

The enzyme of the invention may have a cellulose-binding domain consisting of the following amino acid sequence (I):

Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Gln-Cys-Gly-Gly-Xaa-Xaa-Xaa-Xaa-Gly-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Asn-Xaa-Xaa-Tyr-Xaa-Gln-Cys-Xaa (I) (SEQ ID NO: 18)

wherein Xaa is independently any amino acid residue; Xaa's at positions 20, 21, 22, 23, 24, 30 and 31 may be independently absent; preferably, Xaa at position 24 is absent; and one of Xaa at position 11 or 33 is Lys and the other is any amino acid residue except Lys.

Preferably, the cellulose binding domain of the enzyme of the invention may consists of the following amino acid sequence (II):

Cys-Ser-Xaa-Xaa-Tyr-Xaa-Gln-Cys-Gly-Gly-Xaa-Xaa-Trp-Xaa-Gly-Pro-Thr-Cys-Cys-Xaa-Xaa-Gly-Xaa-Thr-Cys-Xaa-Xaa-Xaa-Xaa-Asn-Xaa-Xaa-Tyr-Ser-Gln-Cys-Xaa (II) (SEQ ID NO: 19)

wherein Xaa is independently any amino acid residue; and Xaa's at positions 20, 21, 23, 29 and 30 may be independently absent.

Preferably, one of Xaa at position 11 or 32 in above amino acid sequence (II) may be Lys and the other may be any amino acid residue except Lys.

More preferably, the cellulose binding domain of the enzyme of the invention may

consists of the following amino acid sequence (III):

Cys-Ser-X1-X2-Tyr-X3-Gln-Cys-Gly-Gly-X4-X5-Trp-X6-Gly-Pro-Thr-Cys-Cys-X7-X8-Gly-X9-Thr-Cys-X10-X11-X12-X13-X14-Asn-X15-X16-Tyr-Ser-Gln-Cys-X17 (III)
(SEQ ID NO: 20)

wherein:

X1 is Lys, Ser or Gln;
X2 is Leu, Ala, Val or Gly;
X3 is Gly, Tyr or Ser;
X4 is Lys or Ile;
X5 is Asn, Asp, Gly or Met;
X6 is Asn, Asp, Ser or Thr;
X7 is Glu, Asp or Thr;
X8 is Ser or Ala;
X9 is Ser or Phe;
X10 is Lys or Val;
X11 is Val, Asp, Ala or Gly;
X12 is Ser, Tyr, Gln or Ala;
X13 is Pro, Glu or Lys, or is absent;
X14 is Asp, Gly or Asn, or is absent;
X15 is Asp, Pro, Lys or Glu;
X16 is Tyr, Phe or Trp;
X17 is Leu, Val or Ile; and

one of X4 or X15 is Lys and the other is any amino acid residue except Lys.

The enzyme of the invention derived from the genus *Rhizopus* may have a cellulose-binding domain consisting of the following amino acid sequence (IV):

Cys-Ser-Lys-X21-Tyr-X22-Gln-Cys-Gly-Gly-Lys-X23-Trp-X24-Gly-Pro-Thr-Cys-Cys-Glu-Ser-Gly-Ser-Thr-Cys-X25-X26-X27-X28-X29-Asn-X30-X31-Tyr-Ser-Gln-Cys-X32
(IV) (SEQ ID NO: 21)

wherein:

X21 is Leu or Ala;

X22 is Gly or Tyr;
 X23 is Asn or Asp;
 X24 is Asn or Asp;
 X25 is Lys or Val;
 X26 is Val or Asp;
 X27 is Ser or Tyr;
 X28 is Pro, or is absent;
 X29 is Asp, or is absent;
 X30 is Asp or Pro;
 X31 is Tyr or Phe; and
 X32 is Leu or Val.

Preferably, the cellulose binding domain consisting of the amino acid sequence (IV) may consists of any one of the amino acid sequences of SEQ ID NOS: 22, 23, and 24.

The enzyme of the invention derived from the genus *Mucor* may have a cellulose-binding domain consisting of the following amino acid sequence (V):
 Cys-Ser-Ser-Val-Tyr-X41-Gln-Cys-Gly-Gly-Ile-Gly-Trp-X42-Gly-Pro-Thr-Cys-Cys-X43-X
 44-Gly-Ser-Thr-Cys-X45-Ala-Gln-X46-X47-Asn-Lys-Tyr-Tyr-Ser-Gln-Cys-X48 (V)
 (SEQ ID NO: 25)

wherein:

X41 is Gly or Ser;
 X42 is Ser or Thr;
 X43 is Glu or Asp;
 X44 is Ser or Ala;
 X45 is Val or Lys;
 X46 is Glu or Lys;
 X47 is Gly or Asp; and
 X48 is Leu or Ile.

The cellulose binding domain consisting of the amino acid sequence (V) may comprise the amino acid sequence of SEQ ID NO: 26 or 27.

The enzyme of the invention derived from the genus *Phycomyces* may have a

cellulose binding domain comprising the amino acid sequence of SEQ ID NO: 28.

(vii) Linker Region and Catalytic Domain

It is known that endoglucanases have a catalytic domain, which cleaves cellulose. The amino acid region, which binds a catalytic domain to a cellulose-binding domain, is called a linker region. Endoglucanases belonging to family 45 are confirmed to have a conserved consensus sequence (Ser or Thr or Ala)-Thr-Arg-Tyr-(Trp or Tyr or Phe)-Asp-Xaa-Xaa-Xaa-Xaa-Xaa-(Cys or Ala) (SEQ ID NO: 29) in an upstream region within their catalytic domains. The present inventors have found that deletion of a specific region upstream of this consensus sequence (i.e., a specific part of the linker region) eliminates lyocell fuzz removal activity (Example D9), and further found that a novel sequence Tyr-Xaa-Xaa-Xaa-Ser-Gly-Gly-Xaa-Ser-Gly (SEQ ID NO: 30) common in *Zygomycotina*-derived 6 endoglucanases is present within the region.

The enzyme of the invention may comprise a part of its linker region consisting of the following amino acid sequence (VI):

Tyr-Xaa-Xaa-Xaa-X51-Gly-Gly-Xaa-X52-Gly (VI) (SEQ ID NO: 31)

wherein Xaa is independently any amino acid residue; X51 and X52 are independently Ser or Thr; and preferably, both X51 and X52 are Ser.

Preferably, the part of the linker region may consist of the following amino acid sequence (VII):

Tyr-X61-Xaa-X62-X51-Gly-Gly-Xaa-X52-Gly (VII) (SEQ ID NO: 32)

wherein:

Xaa is any amino acid residue; preferably, Xaa at position 3 is Ala, Ile, Pro or Val; and Xaa at position 8 is Ala, Phe or Lys;

X51 and X52 are independently Ser or Thr; preferably, both X51 and X52 are Ser;

X61 is Lys or Ser; and

X62 is Ile or Val.

More preferably, the part of the linker region may comprise any one of the sequences as shown in SEQ ID NOS: 33, 34, 35, 36 and 37.

The enzyme according to the invention is characterized by comprising a cellulose-binding domain, a linker region and a catalytic domain located in this order in the

direction from the N-terminus to the C-terminus.

The "part of the linker region" used herein means a part located within the linker region and located close to the N-terminus of the catalytic domain. Specifically, the C-terminus amino acid of this part of the linker region is located 6-14 amino acids, preferably 7-11 amino acids, and more preferably 9 amino acids upstream of the Asp residue in the consensus sequence (Ser or Thr or Ala)-Thr-Arg-Tyr-(Trp or Tyr or Phe)-Asp-Xaa-Xaa-Xaa-Xaa-Xaa-(Cys or Ala) (SEQ ID NO: 29) conserved in the catalytic domain.

(viii) Original Source

The enzymes according to the invention can be obtained from *Zygomycotina*. Specifically, they can be obtained from microorganisms of the genus *Rhizopus* (e.g., *Rhizopus oryzae*), the genus *Mucor* (e.g., *Mucor circinelloides*) or the genus *Phycomyces* (e.g., *Phycomyces nitens*).

According to another aspect of the invention, there is provided an enzyme, which comprises a cellulose-binding domain consisting of any one of the amino acid sequences (I) to (V) and shows endoglucanase activity.

According to another aspect of the invention, there is provided an enzyme which comprises a part of its linker region consisting of the amino acid sequence (VI) or (VII) and shows endoglucanase activity.

According to another aspect of the invention, there is provided an enzyme which comprises a cellulose binding domain consisting of any one of the amino acid sequences (I) to (V) and a part of its linker region consisting of the amino acid sequence (VI) or (VII), and exhibits endoglucanase activity.

According to another aspect of the invention, there is provided an endoglucanase having the following characteristics:

- i) belonging to family 45;
- ii) being derived from a filamentous fungus; and
- iii) having a cellulose-binding domain located on its N-terminal side.

An endoglucanase "belonging to family 45" refers to an endoglucanase which has the conserved consensus sequence (Ser or Thr or Ala)-Thr-Arg-Tyr-(Trp or Tyr or

Phe)-Asp-Xaa-Xaa-Xaa-Xaa-Xaa-(Cys or Ala) (SEQ ID NO: 29) in its catalytic domain (NiceSite View of PROSITE: PDOC00877 or PS01140, PROSITE Database of protein families and domains).

As an endoglucanase "derived from a filamentous fungus and belonging to family 45", enzymes such as EGV, NCE4 and *egl5* (Saloheimo, A. et al., Molecular Microbiology 13:219-228, 1994) are known. In all of these enzymes, the cellulose-binding domain is located on their C-terminal side (Schulein, M., Biochemical Society Transactions 26:164-167, 1998). However, *Zygomycotina*-derived 6 endoglucanases according to the invention belong to family 45 and have a completely novel structure in which the cellulose binding domain is located on their N-terminal side.

Specific examples of endoglucanases "belonging to family 45" according to the invention include an enzyme comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11 and exhibiting endoglucanase activity; a modified protein thereof exhibiting endoglucanase activity; and a homologue of the enzyme or the modified protein which still retains the conserved consensus sequence (Ser or Thr or Ala)-Thr-Arg-Tyr-(Trp or Tyr or Phe)-Asp-Xaa-Xaa-Xaa-Xaa-Xaa-(Cys or Ala) (SEQ ID NO: 29) in its catalytic domain. Specific examples of cellulose binding domains and original sources may include the cellulose binding domains and origin sources described above.

According to another aspect of the invention, there is provided a protein comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11 as an enzyme exhibiting endoglucanase activity. Hereinafter, the proteins having the amino acid sequences of SEQ ID NOS: 1, 3, 5, 7, 9 and 11 are referred to as endoglucanases RCE I, RCE II, RCE III, MCE I, MCE II and PCE I, respectively.

The present invention encompasses not only the polypeptides having the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11 but also modified proteins thereof. In the present invention, the modified protein means a protein which comprises the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11 having modification such as addition, insertion, deletion or substitution in one or more amino acids (e.g., one to several ten amino acids; specifically, one to about 50, preferably one to about 30, more preferably one to about 9 amino acids) and which still retains endoglucanase activity.

Examples of the modified protein include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that asparagines(Asn)-linked oligosaccharide chains are not added thereto as described later.

Examples of the modified protein further include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 whose cellulose binding domain is modified. More specifically, examples of the modified protein include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that its cellulose binding domain represents one of the amino acid sequences (I) to (V) and which may have a modification(s) in regions other than the cellulose binding domain. The number of amino acids, which may be modified in the cellulose-binding domain, is one to about 28, preferably one to about 17.

Examples of the modified protein further include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 in which a part of its linker region is modified. More specifically, examples of the modified protein include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that a part of its linker region represents the amino acid sequence (VI) to (VII) and which may have a modification(s) in regions other than the part of the linker region. The number of amino acids, which may be modified in the linker region, is one to about 6, preferably one to about 4.

Examples of the modified protein further include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 in which its cellulose binding domain and a part of its linker region are modified. More specifically, examples of the modified protein include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that its cellulose binding domain represents one of the amino acid sequences (I) to (V) and yet modified so that a part of its linker region represents the amino acid sequence (VI) or (VII), and which may have a modification(s) in regions other than the cellulose binding domain and the part of the linker region. The number of amino acids, which may be modified in the cellulose-binding domain, is one to about 28, preferably one to about 17. The number of amino acids, which may be modified in the linker region, is one to about 6, preferably one to about 4.

Further, examples of the modified protein include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified in a region(s) other than the cellulose binding domain (CBD) and a part of the linker region. The number of amino acids which may be modified in a region(s) other than the CBD and the part of the linker region is one to about 30, preferably one to about 15. Of these, the number of amino acids, which may be modified in the catalytic domain, is one to about 20, preferably one to about 10.

Further, examples of the modified protein include a protein consisting of an amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified in a region(s) other than the CBD, a part of the linker region and the catalytic domain (CAD). The number of amino acids which may be modified in a region(s) other than the CBD, the part of the linker region and the CAD is one to about 10, preferably one to about 5.

The locations (i.e., amino acid positions) of the CBD(s), the part of the linker region and the CAD in each of SEQ ID NOS: 1, 3, 5, 7, 9 and 11 are shown in the table below.

	CBD	Part of Linker Region	CAD
SEQ ID NO: 1	3~38	99~108	109~315
SEQ ID NO: 3	3~38, 50~85	127~136	137~343
SEQ ID NO: 5	3~40	122~131	132~337
SEQ ID NO: 7	3~40	104~113	114~316
SEQ ID NO: 9	3~40, 52~89	153~162	163~365
SEQ ID NO: 11	3~40	115~124	125~327

Further, the present invention not only encompasses polypeptides having the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11 and modified proteins thereof, but also encompasses homologues of the polypeptides and the modified proteins. The term "homologue" used herein means a polypeptide which has an amino acid sequence encoded by a gene (nucleotide sequence) that hybridizes with a gene (nucleotide sequence) encoding the amino acid sequence of SEQ ID NO: 1, 3, 5, 7, 9 or 11 "under limited conditions", and which has endoglucanase activity. The term "limited conditions" used herein means

conditions controlled to such an extent that while a probe comprising a nucleotide sequence encoding a part or all of the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11 or the modified version thereof hybridizes with a gene encoding the homologue, this probe does not hybridize with the gene of endoglucanase NCE4 disclosed in WO98/03640 nor with the gene of endoglucanase SCE3 disclosed in WO98/54332 gene (provided that equal amounts of NCE4 gene, SCE3 gene and the gene encoding the homologue are used in the hybridization). More specifically, conditions as described below may be given, for example. Briefly, the full length of the DNA sequence as shown in SEQ ID NO: 2 is labeled and provided as a probe. Then, according to the protocol of ECL direct DNA/RNA labeling detection system (Amersham), the probe is added after 1 hr pre-hybridization (at 42°C). After 15 hr hybridization (at 42°C), the washing with 0.4% SDS, 6 M urea-added 0.5xSSC (SSC: 15 mM trisodium citrate, 150 mM sodium chloride) at 42°C for 20 min is repeated twice, and then the washing with 5xSSC at room temperature for 10 min is repeated twice.

The enzyme of the invention may be isolated and purified from a microorganism as described in Examples A1-3.

Alternatively, the enzyme of the invention may be obtained by expressing a nucleotide sequence encoding the enzyme in an appropriate host by recombinant gene technology and isolating/purifying the resultant protein.

The enzyme of the invention also includes a recombinant enzyme consisting of the above-described cellulose binding domain, the specific part of the linker region and any catalytic domain. Such recombinant enzymes may be produced, for example, according to the method of Tomme, P. et al., J. Biotriol. 177:4356-4363, 1995.

Endoglucanase Genes

According to the invention, there is provided a nucleotide sequence encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11; a modified protein thereof; or a homologue of the protein or the modified protein. If an amino acid sequence of a protein is given, DNA sequences encoding the same are easily determined. Thus, various nucleotide sequences encoding a protein comprising the amino

acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11; a modified protein thereof; or a homologues of the protein or the modified protein may be selected.

The nucleotide sequence of according to the present invention may be a naturally occurring sequence or a fully synthetic sequence. Alternatively, the nucleotide sequence may be a sequence synthesized utilizing a part of a naturally occurring sequence. Typically, the nucleotide sequence of the invention is obtained from a chromosomal or cDNA library derived from a microorganism, such as *Mucor circinelloides* or *Phycomyces nitens*, by conventional methods in the art of genetic engineering, e.g., screening with an appropriate DNA probe prepared based on information concerning a partial amino acid sequence.

Hereinbelow, endoglucanases RCE I, RCE II, RCE III, MCE I, MCE II and PCE I, and genes thereof will be described in more detail.

(1) Endoglucanase RCE I and Genes thereof

Endoglucanase RCE I of the invention is an enzyme having the amino acid sequence spanning from position 1 to position 315 of SEQ ID NO: 1 and having endoglucanase activity. The amino acid sequence spanning from position -23 to position -1 of SEQ ID NO: 1 or a part thereof may be added to the N-terminus of the above protein. The polypeptide to which this sequence is added is included within the invention as a modified peptide of endoglucanase RCE I. Since this amino acid sequence spanning from position -23 to position -1 is believed to be a signal peptide for secretion, a part of the sequence means a partial sequence retaining the signal peptide activity as well as a sequence remaining at the N-terminus as a result of some difference that occurred in the site of processing depending on the type of the host.

According to the present invention, there are provided endoglucanase RCE I genes encoding the amino acid sequence of SEQ ID NO: 1. A typical sequence of these genes comprises a part or all of the nucleotide sequence of SEQ ID NO: 2. The nucleotide sequence of SEQ ID NO: 2 contains an open reading frame staring with ATG at positions 1-3 and ending with TAA at positions 1015-1017. The nucleotide sequence of positions 70-72 corresponds to the N-terminal amino acid in the above-described mature protein consisting of 315 residues.

(2) Endoglucanase RCE II and Genes thereof

Endoglucanase RCE II of the invention is an enzyme having the amino acid sequence spanning from position 1 to position 343 of SEQ ID NO: 3 and having endoglucanase activity. The amino acid sequence spanning from position -23 to position -1 of SEQ ID NO: 1 or a part thereof may be added to the N-terminus of the above protein. The polypeptide to which this sequence is added is included within the invention as a modified peptide of endoglucanase RCE II. Since this amino acid sequence spanning from position -23 to position -1 is believed to be a signal peptide, a part of the sequence means a partial sequence retaining the signal peptide activity as well as a sequence remaining at the N-terminus as a result of some difference that occurred in the site of processing depending on the type of the host.

According to the present invention, there are provided endoglucanase RCE II genes encoding the amino acid sequence of SEQ ID NO: 3. A typical sequence of these genes comprises a part or all of the nucleotide sequence of SEQ ID NO: 4. The nucleotide sequence of SEQ ID NO: 4 contains an open reading frame starting with ATG at positions 1-3 and ending with TAA at positions 1099-1101. The nucleotide sequence of positions 70-72 corresponds to the N-terminal amino acid in the above-described mature protein consisting of 343 residues.

(3) Endoglucanase RCE III and Genes thereof

Endoglucanase RCE III of the invention is an enzyme having the amino acid sequence spanning from position 1 to position 337 of SEQ ID NO: 5 and having endoglucanase activity. The amino acid sequence spanning from position -23 to position -1 of SEQ ID NO: 1 or a part thereof may be added to the N-terminus of the above protein. The polypeptide to which this sequence is added is included within the invention as a modified peptide of endoglucanase RCE III. Since this amino acid sequence spanning from position -23 to position -1 is believed to be a signal peptide, a part of the sequence means a partial sequence retaining the signal peptide activity as well as a sequence remaining at the N-terminus as a result of some difference that occurred in the site of processing depending on the type of the host.

According to the present invention, there are provided endoglucanase RCE III genes

encoding the amino acid sequence of SEQ ID NO: 5. A typical sequence of these genes comprises a part or all of the nucleotide sequence of SEQ ID NO: 6. The nucleotide sequence of SEQ ID NO: 6 contains an open reading frame starting with ATG at positions 1-3 and ending with TAA at positions 1081-1083. The nucleotide sequence of positions 70-72 corresponds to the N-terminal amino acid in the above-described mature protein consisting of 337 residues.

(4) Endoglucanase MCE I and Genes thereof

Endoglucanase MCE I of the invention is an enzyme having the amino acid sequence spanning from position 1 to position 316 of SEQ ID NO: 7 and having endoglucanase activity. The amino acid sequence spanning from position -22 to position -1 of SEQ ID NO: 7 or a part thereof may be added to the N-terminus of the above protein. The polypeptide to which this sequence is added is included within the invention as a modified peptide of endoglucanase MCE I. Since this amino acid sequence spanning from position -22 to position -1 is believed to be a signal peptide for secretion, a part of the sequence means a partial sequence retaining the signal peptide activity as well as a sequence remaining at the N-terminus as a result of some difference that occurred in the site of processing depending on the type of the host.

According to the present invention, there are provided endoglucanase MCE I genes encoding the amino acid sequence of SEQ ID NO: 7. A typical sequence of these genes comprises a part or all of the nucleotide sequence of SEQ ID NO: 8. The nucleotide sequence of SEQ ID NO: 8 contains an open reading frame starting with ATG at positions 1-3 and ending with TAA at positions 1015-1017. The nucleotide sequence of positions 67-69 corresponds to the N-terminal amino acid in the above-described mature protein consisting of 316 residues.

(5) Endoglucanase MCE II and Genes thereof

Endoglucanase MCE II of the invention is an enzyme having the amino acid sequence spanning from position 1 to position 365 of SEQ ID NO: 9 and having endoglucanase activity. The amino acid sequence spanning from position -22 to position -1 of SEQ ID NO: 9 or a part thereof may be added to the N-terminus of the above protein. The polypeptide to which this sequence is added is included within the invention as a modified

peptide of endoglucanase MCE II. Since this amino acid sequence spanning from position -22 to position -1 is believed to be a signal peptide, a part of the sequence means a partial sequence retaining the signal peptide activity as well as a sequence remaining at the N-terminus as a result of some difference that occurred in the site of processing depending on the type of the host.

According to the present invention, there are provided endoglucanase MCE II genes encoding the amino acid sequence of SEQ ID NO: 9. A typical sequence of these genes comprises a part or all of the nucleotide sequence of SEQ ID NO: 10. The nucleotide sequence of SEQ ID NO: 10 contains an open reading frame starting with ATG at positions 1-3 and ending with TAA at positions 1162-1164. The nucleotide sequence of positions 67-69 corresponds to the N-terminal amino acid in the above-described mature protein consisting of 365 residues.

(6) Endoglucanase PCE I and Genes thereof

Endoglucanase PCE I of the invention is an enzyme having the amino acid sequence spanning from position 1 to position 327 of SEQ ID NO: 11 and having endoglucanase activity. The amino acid sequence spanning from position -19 to position -1 of SEQ ID NO: 11 or a part thereof may be added to the N-terminus of the above protein. The polypeptide to which this sequence is added is included within the invention as a modified peptide of endoglucanase PCE I. Since this amino acid sequence spanning from position -19 to position -1 is believed to be a signal peptide, a part of the sequence means a partial sequence retaining the signal peptide activity as well as a sequence remaining at the N-terminus as a result of some difference that occurred in the site of processing depending on the type of the host.

According to the present invention, there are provided endoglucanase PCE I genes encoding the amino acid sequence of SEQ ID NO: 11. A typical sequence of these genes comprises a part or all of the nucleotide sequence of SEQ ID NO: 12. The nucleotide sequence of SEQ ID NO: 12 contains an open reading frame starting with ATG at positions 1-3 and ending with TAA at positions 1039-1041. The nucleotide sequence of positions 58-60 corresponds to the N-terminal amino acid in the above-described mature protein consisting of 327 residues.

Expression Vectors and Transformed Microorganisms

According to the invention, there is provided an expression vector replicable in a host microorganism, which comprises a nucleotide sequence encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11; a modified protein thereof; or a homologue of the protein or the modified protein operably linked thereto. This expression vector is an autonomously replicating vector and may be constructed based on, for example, a plasmid that exists as an extrachromosomal entity and replicates independently of the chromosome. Alternatively, the expression vector may be a vector, which is integrated into the genome of the microorganism host upon introduction therein and replicated together with the chromosome into which it has been incorporated. For the construction of the vector of the invention, conventional procedures and methods used in the field of genetic engineering may be used.

For the expression of a protein with desired activity upon introduction into the host microorganism, it is desirable that the expression vector of the invention contains DNA sequences to regulate the expression and gene markers, etc. for the selection of transformed microorganism, in addition to the DNA sequence of the invention. Examples of expression regulatory DNA sequences include promoters, terminators and DNA sequences encoding signal peptides. A promoter, which may be used in the invention, is not particularly limited as long as it shows transcription activity in the host microorganism. It may be obtained as a DNA sequence, which controls the expression of a gene encoding a protein homogeneous or heterogeneous to the host microorganism. A signal peptide, which may be used in the invention, is not particularly limited as long as it contributes to the secretion of protein in the host microorganism. It may be obtained from DNA sequences derived from a gene encoding a protein homogeneous or heterogeneous to the host microorganism. A gene marker, which may be used in the invention, may be appropriately selected depending on the method of selection of transformants. For example, genes encoding drug resistance or genes complementing auxotrophy may be used.

According to the present invention, there is further provided a microorganism transformed with the expression vector. This host-vector system is not particularly limited.

Examples of useful host-vector system include a system using a microorganism such as *Escherichia coli*, actinomycetes, yeast or filamentous fungus; and a fusion protein expression system using such a microorganism.

Transformation of microorganisms with the expression vector of the invention may be performed by conventional methods in the art.

Further, the resultant transformant may be cultivated in an appropriate medium followed by isolation of the protein of the invention from the resultant cultivation broth. Thus, according to another aspect of the invention, there is provided a method of producing the novel protein of the invention. The cultivation condition of the transformant may be essentially the same as those for the microorganism used as the host. As to the method of recovering the protein of interest from the cultivation broth of the transformant, conventional methods in the art may be used.

According to a preferred aspect of the invention, there are provided yeast cells capable of expressing the endoglucanase encoded by the DNA sequence of the invention. Examples of yeast cells, which may be used in the invention, include microorganisms belonging to the genus *Saccharomyces*, the genus *Hansenula* or the genus *Pichia* (e.g., *Saccharomyces cerevisiae*).

Furthermore, according to the present invention, there is provided a method of improving an endoglucanase produced by yeast transformed with the expression vector of the invention when the endoglucanase does not exhibit an activity available to an appropriate use in the invention. Examples of activities available to appropriate uses according to the invention include the activity that can be used in the removal of fuzz from cellulose-containing fabrics.

It was reported by Van Arsdell, J.N. et al. that when a heterogeneous protein is expressed in yeast cells, sometimes, over-glycosylation (i.e., excessive addition of sugar chains) occurs (Van Arsdell, J.N., 1987, *Bio Technology*, 5, 60-64). Therefore, in order to express a protein with a desired activity in such yeast cells, control of glycosylation addition may be necessary. As one example of such control, the present invention provides a method in which the Asparagine(Asn)-linked glycosylation site(s) of an endoglucanase is/are modified to thereby create a mutant endoglucanase to which

Asn-linked oligosaccharide chains will not be added (Examples B9, C6, C10 and E4).

The modification of an endoglucanase consisting of the amino acid sequence of SEQ ID NO: 1, 3, 5, 7, 9 or 11 into a mutant endoglucanase to which Asn-linked oligosaccharide chains will not be added may be the replacement of Asn, Ser and/or Thr in the Asn-linked glycosylation site(s) represented by the sequence Asn-Xaa-Ser/Thr with other amino acid residue. Specifically, the modification may be the replacement of Asn with Asp or Gln; the replacement of Ser or Thr with Ala, Gly or Leu; or the replacement of Xaa with Pro in the glycosylation site(s).

As described in Examples C10 and C11, enzyme activity can be improved greatly by modifying even one Asn-linked glycosylation site adjacent to the cellulose-binding domain. Examples of mutant endoglucanases to which Asn-linked oligosaccharide chains will not be added include endoglucanases consisting of one of the following amino acid sequences:

A modified amino acid sequence represented by SEQ ID NO: 1 where the amino acid residue at position 45 or 47 is replaced by other amino acid residue;

A modified amino acid sequence represented by SEQ ID NO: 3 where the amino acid residue at position 45 or 47 is replaced by other amino acid residue;

A modified amino acid sequence represented by SEQ ID NO: 5 where the amino acid residue at position 44 or 46 is replaced by other amino acid residue;

A modified amino acid sequence represented by SEQ ID NO: 7 where the amino acid residue at position 50 or 52 is replaced by other amino acid residue; and

A modified amino acid sequence represented by SEQ ID NO: 9 where the amino acid residue at position 99 or 101 is replaced by other amino acid residue.

Further examples of mutant endoglucanases to which Asn-linked oligosaccharide chains will not be added include endoglucanases consisting of one of the following amino acid sequences:

A modified amino acid sequence represented by SEQ ID NO: 1 where the amino acid residue at position 45 or 47 and the amino acid residue(s) at position 90 or 92 and/or 130 or 132 are replaced by other amino acid residues;

A modified amino acid sequence represented by SEQ ID NO: 3 where the amino acid residue at position 45 or 47, and the amino acid residue(s) at position 92 or 94, 119 or

121, 122 or 124 and/or 158 or 160 are replaced by other amino acid residues; and

A modified amino acid sequence represented by SEQ ID NO: 5 where the amino acid residue at position 44 or 46 and the amino acid residue(s) at position 49 or 51, 121 or 123 and/or 171 or 173 are replaced by other amino acid residues.

More specifically, examples of mutant endoglucanases to which Asn-linked oligosaccharide chains will not be added include endoglucanases consisting of one of the following amino acid sequences:

A modified amino acid sequence represented by SEQ ID NO: 1 where Ser at position 47 is replaced by Ala; Ser at position 92 is replaced by Gly; and Asn at position 130 is replaced by Asp;

A modified amino acid sequence represented by SEQ ID NO: 3 where Ser at position 47 is replaced by Ala; Asn at position 92 is replaced by Gln; Ser at position 121 is replaced by Leu; Asn at position 122 is replaced by Asp; and Asn at position 158 is replaced by Asp;

A modified amino acid sequence represented by SEQ ID NO: 5 where Asn at position 44 is replaced by Asp; and Asn at position 121 is replaced by Lys;

A modified amino acid sequence represented by SEQ ID NO: 7 where Ser at position 52 is replaced by Gly; and

A modified amino acid sequence represented by SEQ ID NO: 9 where Ser at position 101 is replaced by Gly.

In the control of glycosylation as described above, it is also possible to use host yeast cells of which glycosylation capacity has been limited (or even deleted) by mutagenesis techniques known in the art.

As a most suitable method for producing the endoglucanase of the invention, a method is provided in which the endoglucanase is expressed in filamentous fungi belonging to *Deuteromycotina*. When the enzyme is expressed in filamentous fungi belonging to *Deuteromycotina*, it is desirable to use a codon-optimized gene in which codons have been optimized in conformity with the codon usage in host filamentous fungi. In the present invention, a "codon-optimized gene" means a gene having such a DNA sequence as obtained by substituting codons in a DNA sequence encoding a protein based on

information on frequently used codons in a host filamentous fungus.

Examples of most suitable codon-optimized genes in the invention include genes which do not contain intron recognition sequences or which seldom contain such sequences. The term "intron recognition sequence" used herein means a DNA sequence, which may be recognized by filamentous fungi belonging to *Deuteromycotina* as an intron. More specifically, the intron recognition sequence means a DNA sequence such as GTAGN, GTATN, GTAAN, GTACGN, GTGTN, GCACGN or GTTCGN. The absence of these DNA sequences leads to an improvement in the stability of mRNA that is the transcript of a gene of interest.

According to the present invention, it is possible to obtain an industrially preferable yield of the endoglucanase by totally synthesizing the above-described codon-optimized gene, integrating it into an expression vector and transforming a host filamentous fungus with the vector. The host filamentous fungus in the invention may belong to the genus *Humicola*, *Aspergillus*, *Trichoderma*, *Acremonium* or *Fusarium*. Preferable examples of them include *Humicola insolens*, *Aspergillus niger* and *Trichoderma viride*.

One example of the codon-optimized genes used in the invention is codon-optimized endoglucanase RCE I gene. This gene is a codon-optimized gene encoding endoglucanase RCE I having the amino acid sequence as shown in SEQ ID NO: 1. A typical sequence of this gene comprises a part or all of the nucleotide sequence as shown in SEQ ID NO: 13. The nucleotide sequence as shown in SEQ ID NO: 13 contains an open reading frame starting with ATG at positions 16-18 and ending with TAA at positions 1030-1032. The nucleotide sequence of positions 85-87 corresponds to the N-terminal amino acid of the above-mentioned mature protein of 315 residues.

Uses of Cellulases/Cellulase Preparations

According to another aspect of the invention, there are provided cellulase preparations comprising the endoglucanase of the invention, modified protein thereof or homologue thereof. The cellulase preparation of the invention may be prepared by mixing the endoglucanase of the invention, modified protein thereof or homologue thereof with components generally contained in cellulase preparations, such as excipients (e.g., lactose,

sodium chloride, sorbitol); surfactants; and preservatives. The cellulase preparation of the invention may be prepared into an appropriate form such as powder or liquid formulation, or granules.

According to the present invention, there is further provided a method of reducing a speed at which cellulose-containing fabrics become fuzzy or reducing fuzzing in such a fabric; or a method of reducing a speed at which cellulose-containing fabrics become stiff or reducing stiffness in such a fiber. Each of these methods comprises a step of treating cellulose-containing fabrics with the endoglucanase or the cellulase preparation of the invention.

According to the present invention, there are further provided a method of color clarification of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing fabrics with the endoglucanase or the cellulase preparation; and a method of providing colored cellulose-containing fabrics with partial color change, i.e., a method of providing colored cellulose-containing fabrics with an appearance of stone-washed material, which method comprises a step of treating the colored cellulose-containing fabrics with the endoglucanase or the cellulase preparation of the invention.

The methods of the invention described above may be carried out by treating cellulose-containing fabrics during washing. Alternatively, on some occasions, the treatment of fabrics may be carried out during soaking or rinsing by adding the endoglucanase or the cellulase preparation of the invention into water where the fabric is soaked or to be soaked.

Conditions such as the contact temperature or the amount of endoglucanase may be appropriately decided considering other various conditions. For example, in the treatment for reducing a speed at which cellulose-containing fabrics become fuzzy or reducing fuzzing in such a fabric, the fabric can be treated with the endoglucanase at a protein concentration of 0.2-1 mg/L at about 45-55°C.

In weight loss treatment of cellulose-containing fabrics to improve its touch and appearance, the fabrics can be treated with the endoglucanase at a protein concentration of 5-100 mg/L at about 45-55°C.

Further, the fabrics can be treated with the endoglucanase at a protein concentration of 2-10mg/L at about 45-55°C to provide colored cellulose-containing fabrics with partial color change.

By using the endoglucanase or the cellulase preparation of the invention in detergent compositions, improvement can be made in granular soil removal, color clarification-, defuzzing, depilling and reduction of stiffness.

The detergent composition of the invention may also contain a surfactant (which may be anionic, nonionic, cationic, amphoteric or zwitterionic surfactant, or a mixture thereof). Further, the detergent composition of the invention may contain other detergent components known in the art, such as builders, bleaching agents, bleaching activators, corrosion inhibitors, sequestering agents, stain-dissociating polymers, aromatics, other enzymes, enzyme stabilizers, formulation assistants, fluorescent brightening agents, foaming promoters, etc. Examples of representative anionic surfactants include linear alkyl benzene sulfonate (LAS), alkylsulfate (AS), α -olefin sulfonate (AOS), alcohol ethoxy sulfate (AES) and alkali metal salts of natural fatty acids. Examples of nonionic surfactants include alkyl polyethylene glycol ether, nonylphenol polyethylene glycol ether, fatty acid esters of sucrose and glucose, and esters of polyethoxylated alkylglucoside.

It has been found that treating waste paper with the endoglucanase or the cellulase preparation of the invention can deink the paper. Thus, the use of the endoglucanase of the invention in the process of manufacturing recycled paper from waste paper can reduce ink-remaining fiber greatly to thereby improve the whiteness of the waste paper. Examples of waste paper which may be used in the invention include used printed paper such as used newspaper, used magazine paper and low-grade or middle-grade used printed paper containing mechanical pulp and chemical pulp; used wood-free paper composed of chemical pulp; and coated paper thereof. The term "deinking agent" used herein means those drugs commonly used in the deinking of waste paper, including alkali such as NaOH or Na_2CO_3 , soda silicate, hydrogen peroxide, phosphates, anionic or nonionic surfactants, capturing agents such as oleic acid, pH stabilizers as aids, chelating agents, or dispersants.

According to the invention, it has also been found that treating paper pulp with the endoglucanase of the invention can significantly improve the freeness (drainage) of the pulp

without remarkable reduction in its strength. Thus, the present invention provides a method of improving the freeness of paper pulp, comprising a step of treating the paper pulp with the endoglucanase or the cellulase preparation of the invention. Examples of pulp, which can be treated by the method of the invention, include waste paper pulp, recycled board pulp, kraft pulp, sulfite pulp or processed/thermally treated pulp, and other high-yield pulp.

Furthermore, the digestibility of glucans in animal feeds can be improved by using the endoglucanase of the invention in such feeds. Thus, the present invention provides a method of improving the digestibility of animal feeds, comprising a step of treating the animal feed with the endoglucanase or the cellulase preparation of the invention.

EXAMPLES

The present invention will be further described in detail by the following examples but is not limited thereto.

Endoglucanase Activity

Hereinafter, endoglucanase activity means CMCase activity. Further, one unit of "CMCase activity" is defined as the amount of a cellulase enzyme which produces reducing sugars corresponding to one μmol of glucose per minute as determined by measuring amounts of the reducing sugars released from a solution of carboxymethyl cellulose (CMC, Tokyo Kasei Kogyo, Japan) after incubation with the enzyme for a certain period of time.

EXAMPLE A1: Isolation and purification of endoglucanase enzyme from *Rhizopus oryzae*

Rhizopus oryzae strain CP96001 (FERM BP-6889) was subjected to shaker cultivation in a medium (6.0% corn steep liquor, 3.0% wheat bran, 1.0% glucose, 0.5% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.15% CaCO_3) at 28°C . After incubation for 3 days, cells were removed out to provide a cultivation supernatant as a crude cellulase preparation.

An ammonium sulfate solution at a final concentration of 1.25 M was prepared from 80 ml of the crude cellulase preparation and applied at a flow rate of 3.4 ml/min to Macro-Prep Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.25 M ammonium sulfate solution. It was then fractionated by eluting at a flow rate of 5.0 ml/min in a stepwise elution method in which the concentration of ammonium sulfate in deionized water was decreased by 0.25

M each from 1.25 M. Among the fractions, a portion of those fractions obtained at an ammonium sulfate concentration of 0.75 M was found to have a strong activity in the removal of fuzz from lyocell. Therefore, 50 ml of this fraction was isolated. By repeating 150 times the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 12 l of the cultivation supernatant were treated to provide 7.5 l of active fractions.

An ammonium sulfate solution at a final concentration of 1.25 M was prepared from 7.5 l of the active fractions. Among them, 190 ml of the fractions were applied at a flow rate of 2.8 ml/min to Macro-Prep Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories), which had been equilibrated with 1.25 M ammonium sulfate solution. Then, 1.25 M and 1.125 M ammonium sulfate solutions were stepwise applied at a flow rate of 5.0 ml/min. The fractions then eluted with about 20 ml of deionized water were found to have a strong activity in the removal of fuzz from lyocell and therefore pooled. By repeating 40 times the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 7.5 l of the active fractions obtained in the previous step were treated to provide 800 ml of active fractions.

Then, 800 ml of the active fractions were diluted 10 times with 50 mM acetate buffer (pH 4.0) to 8.0 l of a solution, 23 ml of which were applied at a flow rate of 0.9 ml/min to MonoS HR 5/5 cation chromatography (Pharmacia Biotech) that had been equilibrated with 50 mM acetate buffer (pH 4.0). It was then eluted with a linear gradient of Buffer A (50 mM acetate buffer, pH 4.0) and Buffer B (50 mM acetate buffer containing 1 M NaCl, pH 5.2) at a flow rate of 0.9 ml/min. Those fractions, which were found to have a strong activity in the removal of fuzz from lyocell were isolated. The fractionation by MonoS HR 5/5 cation chromatography was repeated 350 times to isolate a purified endoglucanase enzyme RCE I. This RCE I showed a single band in SDS-PAGE and had a molecular weight (MW) of about 40 kD. The SDS-PAGE used NPU-12.5L PAGEL (ATTO Japan) and migration and dyeing were carried out according to the specification attached to the gel. Molecular weight standards used were SDS-PAGE molecular weight standard Low range (BioRad Laboratories).

EXAMPLE A2: Isolation and purification of endoglucanase enzyme from *Mucor*

circinelloides

Mucor circinelloides strain CP99001 (FERM BP-6890) was subjected to shaker cultivation in a medium (3.0% corn steep liquor, 3.0% wheat bran, 3.0% glucose, 0.5% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.15% CaCO_3) at 28°C. After incubation for 3 days, cells were removed out to provide a cultivation supernatant as a crude cellulase preparation.

An ammonium sulfate solution at a final concentration of 1.5 M was prepared from 120 ml of the crude cellulase preparation and applied at a flow rate of 3.0 ml/min to Macro-Prep Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.5 M ammonium sulfate solution. It was then fractionated by eluting at a flow rate of 5.0 ml/min in a stepwise elution method in which the concentration of ammonium sulfate in deionized water was decreased by 0.3 M each from 1.5 M. Among them, those fractions obtained at an ammonium sulfate concentration of 0.6 M were found to have a strong activity in the removal of fuzz from lyocell. Therefore, 64.3 ml of this fraction was isolated. By repeating 14 times the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 1710 ml of the cultivation supernatant was treated to provide 900 ml of active fractions.

An ammonium sulfate solution at a final concentration of 1.5 M was prepared from 300 ml of the active fractions and applied at a flow rate of 3.0 ml/min to Macro-Prep Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.5 M ammonium sulfate solution. Then, 1.5 M and 0.9 M ammonium sulfate solutions were stepwise applied at a flow rate of 5.0 ml/min. The fractions then eluted with about 30 ml of deionized water were found to have a strong activity in the removal of fuzz from lyocell and therefore pooled. By repeating 3 times the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 900 ml of the active fractions obtained in the previous step were treated to provide 90 ml of active fractions.

Then, 90 ml of the active fractions were diluted 10 times with 50 mM acetate buffer (pH 4.0) to 900 ml of a solution, 150 ml of which were applied at a flow rate of 1.0 ml/min to MonoS HR 5/5 cation chromatography (Pharmacia Biotech) that had been equilibrated with 50 mM acetate buffer (pH 4.0). It was then eluted with a linear gradient

of Buffer A (50 mM acetate buffer, pH 4.0) and Buffer B (50 mM acetate buffer containing 1 M NaCl, pH 5.2) at a flow rate of 1.0 ml/min. Those fractions, which were found to have a strong activity in the removal of fuzz from lyocell, were isolated. The fractionation by MonoS HR 5/5 cation chromatography was repeated 6 times to isolate a purified endoglucanase enzyme MCE I. This MCE I showed a single band in SDS-PAGE and had a molecular weight (MW) of about 41 kD. The SDS-PAGE used NPU-12.5L PAGEL (ATTO Japan) and migration and dyeing were carried out according to the specification attached to the gel. Molecular weight standards used were SDS-PAGE molecular weight standard Low range (BioRad Laboratories).

EXAMPLE A3: Isolation and purification of endoglucanase enzyme from *Phycomyces nitens*

Phycomyces nitens strain CP99002 (FERM BP-6891) was subjected to Jar fermentor cultivation in a medium (2.0% corn steep liquor, 3.0% wheat bran, 2.0% Sucrose, 1.0% Yeast extract, 0.05% KH_2PO_4 , 0.03% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.15% CaCl_2 , 0.01% Adecanol) at 28°C, 220 rpm. After incubation for 3 days, the cultivation supernatant from which cells were removed out was concentrated 10 times through ultrafiltration using a membrane with a molecular weight digested of 5,000.

An ammonium sulfate solution at a final concentration of 1.5 M was prepared from 120 ml of the ultrafiltrated concentrate and applied at a flow rate of 3.0 ml/min to Macro-Prep Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.5 M ammonium sulfate solution. It was then fractionated by eluting at a flow rate of 5.0 ml/min in a stepwise elution method in which the concentration of ammonium sulfate in deionized water was decreased by 0.3 M each from 1.5 M. Among them, those fractions obtained at an ammonium sulfate concentration of 0.3 M were found to have a strong activity in the removal of fuzz from lyocell. Therefore, 66 ml of this fraction was isolated. By repeating 10 times the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 1200 ml of the ultrafiltrated concentrate were treated to provide 660 ml of active fractions.

An ammonium sulfate solution at a final concentration of 1.5 M was prepared from 165 ml of the active fractions and applied at a flow rate of 3.0 ml/min to Macro-Prep

Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.5 M ammonium sulfate solution. Then, 1.5 M and 0.75 M ammonium sulfate solutions were stepwise applied at a flow rate of 5.0 ml/min. The fractions then eluted with about 30 ml of deionized water were found to have a strong activity in the removal of fuzz from lyocell and therefore pooled. By repeating 4 times the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 660 ml of the active fractions obtained in the previous step were treated to provide 120 ml of active fractions.

Then, 120 ml of the active fractions were diluted 10 times with 50 mM acetate buffer (pH 4.0) to 1200 ml of a solution, 100 ml of which were applied at a flow rate of 1.0 ml/min to MonoS HR 5/5 cation chromatography (Pharmacia Biotech) that had been equilibrated with 50 mM acetate buffer (pH 4.0). It was then eluted with a linear gradient of Buffer A (50 mM acetate buffer, pH 4.0) and Buffer B (50 mM acetate buffer containing 1 M NaCl, pH 5.2) at a flow rate of 1.0 ml/min. Those fractions, which were found to have a strong activity in the removal of fuzz from lyocell, were isolated. The fractionation by MonoS HR 5/5 cation chromatography was repeated 12 times to isolate a purified endoglucanase enzyme PCE I. This PCE I showed a single band in SDS-PAGE and had a molecular weight (MW) of about 45 kD. The SDS-PAGE used NPU-1.25L PAGEL (ATTO Japan) and migration and dyeing were carried out according to the specification attached to the gel. Molecular weight standards used were SDS-PAGE molecular weight standard Low range (BioRad Laboratories).

EXAMPLE A4: Evaluation of action of RCE I, MCE I and PCE I on regenerated cellulose fabrics by launder meter

Fuzz removal activity on lyocell, representative of regenerated cellulose fabrics, of the purified endoglucanase enzyme RCE I, MCE I and PCE I obtained in Examples A1 to A3 was evaluated in the following manner.

Dyed knitted fabric of lyocell (Toyoshima Japan) was fuzzed in a large washer containing surfactants and rubber balls. Thereafter, the fuzzy knitted fabric of lyocell (Toyoshima Japan, 9 cm x 10 cm, about 2 g in weight) was cylindrically sewn and subjected to fuzz removal treatment with various enzymes under the conditions as set forth below.

The protein concentrations of RCE I, MCE I and PCE I required to completely remove fuzz in the inside of the cylindrical fabric by the treatment were calculated.

The protein concentrations of various endoglucanases were calculated from the peak area at UV 280 nm of respective endoglucanase eluted with a linear gradient from 0% to 80% of acetonitrile concentration in 0.05% TFA (trifluoroacetic acid) at a flow rate of 1.0 ml/min in HPLC analysis using TSK gel TMS-250 column (4.6 mm I.D. x 7.5 cm, Tosoh Japan). The standard used was the purified NCE4 which was analyzed in HPLC under the same conditions, the protein concentration of which had been preliminarily measured by protein assay kit (BioRad Laboratories). The standard used to measure the protein concentration in the protein assay kit was albumin standard (Bovine serum albumin, fraction V, PIERCE). The purified NCE4 was isolated and purified from a cultivation broth of *Humicola insolens* according to the method as described in WO98/03640.

Test machine: Launder Meter L-12 (Daiei Kagaku Seiki MFG, Japan)

Reaction temperature: 55°C for RCE I, and 50°C for MCE I and PCE I

Time: 60 minutes

Reaction volume: 40 ml

Reaction pH: pH 5 (10 mM acetate buffer)

pH 6 (10 mM acetate buffer)

The treating liquid contained 4 rubber balls (about 16 g each) together with the endoglucanase solution.

The results are shown in Table 1 below.

Table 1

Enzyme	pH 5	pH 6
RCE I	0.5 mg/l	0.5 mg/l
MCE I	0.5 mg/l	0.5 mg/l
PCE I	1.4 mg/l	0.9 mg/l

EXAMPLE A5: Evaluation of action of RCE I, MCE I and PCE I on a regenerated cellulose fabric at different pH by launder meter

Dyed fabric of lyocell (Toyoshima Japan) was fuzzed in a large washer containing surfactants and rubber balls. Thereafter, the fuzz removal treatment of lyocell was carried out with RCE I, MCE I and PCE I under the conditions as set forth below, and the protein concentrations of the various endoglucanases required to completely remove fuzz were calculated at each pH. The activity value at each pH is shown in the graph attached by its relative activity as compared with the activity value (100) in the pH region at which the highest activity was seen. As a control, the purified NCE4, which is the endoglucanase component from *Humicola insolens* disclosed in WO98/03640, was evaluated in a similar manner.

The protein concentrations of various endoglucanases were calculated from the peak area at UV 280 nm of respective endoglucanase eluted with a linear gradient from 0% to 80% of acetonitrile concentration in 0.05% TFA (trifluoroacetic acid) at a flow rate of 1.0 ml/min in HPLC analysis using TSK gel TMS-250 column (4.6 mm I.D. x 7.5 cm, Toso Japan). The standard used was a purified NCE4 which was analyzed in HPLC under the same conditions, the protein concentration of which had been preliminarily measured by protein assay kit (BioRad Laboratories). The standard used to measure the protein concentration in the protein assay kit was albumin standard (Bovine serum albumin, fraction V, PIERCE).

Test machine: Launder Meter L-12 (Daiei Kagaku Seiki MFG. Japan)

Reaction temperature: 55°C for NCE4 and RCE I, and 50°C for MCE I and PCE I

Time: 60 minutes

Reaction volume: 40 ml

Reaction pH: pH 4-6 (10 mM acetate buffer)

pH 7-9 (10 mM Tris-HCl buffer)

pH 9-10 (10 mM glycine-sodium hydroxide buffer)

The treating liquid contained 4 rubber balls (about 16 g each) together with the endoglucanase solution.

The results are shown in Fig. 1. As seen from the figure, the optimum pH for RCE I, MCE I and PCE I is 5-7 and these enzymes in pH 5-8 possessed 70% or more of the activity at the optimum pH. On the other hand, the control NCE4 had an optimum pH of 5 and possessed only 30% or less of the activity at the optimum pH in the pH region of 6.2 or more. From these results, it is apparent that RCE I, MCE I and PCE I are significantly highly active in the alkaline conditions.

EXAMPLE A6: Evaluation of decoloring activity of denim dyed cellulose-containing fiber by RCE I

Twelve ounce desized blue jeans pants were subjected to decoloring treatment with the crude cellulase preparation and purified endoglucanase enzyme RCE I obtained in Example A1 under the following conditions.

Test machine: 20 kg Washer (Sanyo Denki Japan, full automatic washing machine SCW5101)

Temperature: 55°C

Time: 60 minutes

pH: 6.2 (6.7 mM phosphate buffer)

The treating liquid contained an appropriate amount of rubber balls together with the cellulase preparation.

Decoloration was measured by using a spectrophotometer (Minolta, CM-525i). First, conditions for observation were set to be D₆₅ as a light source and 2° as a visual field for observation and calibration of L* value (lightness) in L*a*b* color system was effected according to the product manual. Next, the L* values in L*a*b* color system of various samples under the conditions were measured. An increase of L* value (increase in brightness) as compared with a control (untreated fiber), i.e., ΔL^* value, was obtained and the degree of decoloration was evaluated by the ΔL^* value. That is, ΔL^* values were measured at 10 points in each test area (n=10) and an average was calculated. Then, the protein concentration of endoglucanase required to provide a ΔL^* value of 7 was

calculated.

The protein concentration was quantified using bovine serum albumin as a standard in protein assay kit (BioRad Laboratories).

The results are shown in Table 2 below.

Table 2

<u>Sample</u>	<u>Protein concentration</u>
Crude cellulase preparation	80.0 mg/l
<u>RCE I</u>	<u>2.0 mg/l</u>

EXAMPLE A7: Weight loss processing test of RCE I on various fabrics

Various cellulose-containing fabrics(15 cm x 10 cm), the absolute dry weight of which had been preliminarily measured, were subjected to enzyme treatment under the following conditions.

Test machine: Launder Meter L-12 (Daiei Kagaku Seiki MFG. Japan)

Temperature: 55°C

Time: 60 minutes

pH: 6 (10 mM acetate buffer)

The treating liquid contained an appropriate amount of stainless beads (Daiei Kagaku Seiki MFG. Japan) together with RCE I preparation (protein concentration of 8.0 mg/L). The protein concentration was quantified using bovine serum albumin as a standard in protein assay kit (BioRad Laboratories).

The absolute dry weights of fabric were measured before and after the enzyme treatment to calculate the weight loss percentage. The results are shown in Table below.

<u>Fabric tested</u>	<u>Weight reduction (%)</u>
Cotton knit	2.79
Linen	1.49
Rayon	2.83

Polysonic

11.32

lyocell

3.47

EXAMPLE B1: Partial amino acid sequences of RCE I, MCE I and PCE I

(1) Identification of N-terminal amino acid residues

In order to determine the N-terminal amino acid sequences of the purified proteins obtained in Examples A1 to A3, column chromatography (column: C8 220 x 2.1 mm, gradient of from 0.1% TFA, 5% acetonitrile to 0.085% TFA, 70% acetonitrile) was carried out in Model 172 μ preparative HPLC system (Perkin Elmer) to further purify the target protein. It was subjected to protein sequencer Model 492 (Perkin Elmer) to determine the N-terminal amino acid sequence. The resulting sequences are as set forth below.

N-Terminal amino acid sequence of RCE I (SEQ ID NO:14):

Ala-Glu-(Cys)-Ser-Lys-Leu-Tyr-Gly-Gln-(Cys)-Gly-Gly-Lys-Asn-Trp-Asn-

* * * *

Gly-Pro-Thr-(Cys)-(Cys)-Glu-Ser-Gly-Ser-Thr-(Cys)-Lys-Val-Ser-Asn-Asp-

* * *

Tyr-Tyr-Ser-Gln-(Cys)-Leu-Pro-Ser (40 residues)

N-Terminal amino acid sequence of MCE I (SEQ ID NO:15):

Ala-Ser-(Cys)-Ser-Ser-Val-Tyr-Gly-Gln-(Cys)-Gly-Gly-Ile-Gly-Trp-Ser-

Gly-Pro-Thr-(Cys)-(Cys)-Glu (22 residues)

N-Terminal amino acid sequence of PCE I (SEQ ID NO:16):

Ala-Glu-(Cys)-Ser-Gln-Gly-Tyr-Gly-Gln-(Cys)-Gly-Gly-Lys-Met-Trp-Thr-

Gly-Pro-Thr-(Cys)-(Cys)-Thr-Ser (23 residues)

(2) Peptide mapping

RCE I protein purified in (1) above was lyophilized and dissolved in 50 mM Tris-HCl buffer (pH 8.0). Lysyl endopeptidase (Wako Pure Chemical Japan) was added in an amount of about 1/100 mole per mole of protein and reacted at 37°C for 48 hours. This cleavage product was subjected to column chromatography in the aforementioned HPLC system (column: C18 220 x 2.1 mm, gradient of from 0.1% TFA, 5% acetonitrile to 0.085% TFA, 35% acetonitrile) to isolate 5 peptides. The amino acid sequences of the resulting peptide fragments were determined by the aforementioned protein sequencer. The results are as set forth below.

LE-1: Asn-Ala-Asp-Asn-Pro-Ser-Met-Thr-Tyr-Lys (10 residues) (SEQ ID NO:38)

LE-2: Tyr-Ser-Ala-Val-Ser-Gly-Gly-Ala-Ser-Gly (10 residues) (SEQ ID NO:39)

LE-3: Ser-Ala-Ser-Asp-(Cys)-Ser-Ser-Leu-Pro-Ser-Ala-Leu-Gln-Ala-Gly-(Cys)-Lys (17 residues) (SEQ ID NO:40)

LE-4: Tyr-Gly-Gly-Ile-Ser-Ser-Ala-Ser-Asp-(Cys)-Ser-Ser-Leu-Pro-Ser-Ala-Leu-Gln (18 residues) (SEQ ID NO:41)

LE-5: Arg-Phe-Asn-Trp-Phe-Lys (6 residues) (SEQ ID NO:42)

* * * * *

EXAMPLE B2: Isolation of genomic DNA

The genomic DNAs were isolated in the following manner.

Rhizopus oryzae was cultivated in 30 ml of YPD liquid medium (1% yeast extract (Difco), 2% polypeptone (Wako Pure Chemical), 2% sucrose) at 30°C for 40 hours, *Mucor circinelloides* was cultivated in 30 ml of YPD liquid medium (0.5% yeast extract (Difco), 2.4% potato dextrose broth (Difco), 2% sucrose) at 30°C for 18 hours, and *Phycomyces nitens* was cultivated in 30 ml of YPD liquid medium (0.5% yeast extract (Difco), 2.4% potato dextrose broth (Difco), 2% sucrose) at 30°C for 48 hours. Cells were collected from each cultivated broth through a glass filter. The resulting cells were lyophilized, finely crushed in a blender, and dissolved in 8 ml of TE (10 mM Tris-HCl (pH 8.0), 1 mM EDTA) buffer. 4 ml of TE buffer containing 10% SDS was added thereto and incubated at 60°C for 30 minutes. Then, 12 ml of phenol-chloroform-isoamyl alcohol (25:24:1) was

added and shaken vigorously. After centrifugation, the aqueous layer was transferred to another vessel, to which 1 ml of 5 M potassium acetate was added and allowed to stand in ice for one hour or more. After centrifugation, the aqueous layer was transferred to another vessel, to which 2.5 volumes of ethanol were added to precipitate DNA. The precipitate was dried, and then dissolved in 5 ml of TE buffer. Thereafter, 5 μ l of 10 mg/ml ribonuclease A (RNase A) solution were added and incubated at 37°C for one hour. Further, 50 μ l of 20 mg/ml proteinase K solution were added and incubated at 37°C for one hour. Thereafter, 3 ml of polyethylene glycol solution (20% PEG 6000, 2.5 M NaCl) were added to precipitate DNA. The precipitate was dissolved in 500 μ l of TE buffer and extracted twice with phenol-chloroform-isoamyl alcohol followed by ethanol precipitation. The precipitate was washed with 70% ethanol, dried and dissolved in an appropriate amount of TE buffer to prepare a sample.

EXAMPLE B3: Preparation of long chain probe by PCR method

(1) Amplification of target DNA fragment by PCR method

As a DNA probe, a long probe was prepared which was amplified from the total DNA of *Rhizopus oryzae* as a template by PCR method.

As each primer, DNAs were synthesized which corresponded to the N-terminal amino acids and the amino acids of the peptide LE-5 marked by *. The prepared synthetic oligonucleotides had the following sequences:

Rh-N: AARAAYTGGAAYGGXCCNAC (20mer) (SEQ ID NO:43)

Rh-4.3a: TTRAACCARTTRAANCG (17mer) (SEQ ID NO:44)

Rh-4.3b: TTRAACCARTTRAAYCT (17mer) (SEQ ID NO:45)

wherein R is A or G; Y is C or T; N is A, G, C or T; and X is an inosine.

The PCR reaction was carried out under the following conditions: First, two sets of tubes, each of which contained 1 μ M of each of Rh-N and Rh-4.3a primers or 1 μ M of each of Rh-N and Rh-4.3b primers in addition to 1 μ g of the genomic DNA of *Rhizopus oryzae*, were prepared and subjected to thermal denaturation at 95°C for 2 minutes in the presence of dNTPs. Then, Taq polymerase (Recombinant Taq, Takara Shuzo) was added and the reaction conditions of 94°C for 1 minute, 45°C for 2 minutes and 72°C for 3 minutes were repeated 25 times followed by incubation at 72°C for 10 minutes. The PCR

product was subjected to 0.8% agarose gel electrophoresis and the results showed that about 800 bp DNA was amplified only when Rh-N and Rh-4.3b were used as primers.

(2) Subcloning of PCR product

The above mentioned about 800 bp DNA fragment amplified by PCR was recovered by using Sephaglas Band Prep Kit (Pharmacia Biotech) and ligated into pT7 Blue T-vector (Novagen) using DNA ligation kit (Takara Shuzo). The resulting ligation mixture was used to transform *E. coli* competent cells JM109 (Takara Shuzo). The resulting transformant was cultivated and plasmid DNA was recovered by the method described by J. Sambrook in "Molecular Cloning: A Laboratory Manual," 2nd Ed., ed. by Cold Spring Harbor Laboratory Press, New York, 1989, pp. 1.25-1.32. The obtained plasmid DNA was digested with plural restriction enzymes and subjected to 0.8% agarose gel electrophoresis to select those plasmid DNAs into which the about 800 bp fragment had been inserted. The plasmid into which a target PCR product was subcloned was designated as pRD05.

(3) Nucleotide sequence analysis of pRD05

The nucleotide sequence analysis was carried out in the following manner:

The apparatus for nucleotide sequence analysis used was A.L.F. DNA sequencer II (Pharmacia Biotech). The sequencing gel used was an acrylamide support available as Hydrolink Long Ranger (FMC). Various reagents for preparing a gel used (N,N,N',N'-tetramethyl ethylenediamine, urea, and ammonium persulfate) were reagents of A.L.F. grade (Pharmacia Biotech). Autoread Sequencing Kit (Pharmacia Biotech) was used in the nucleotide sequence reading reaction. The conditions for preparing a gel, the reaction conditions, and the electrophoretic conditions were set by referring to the details of each specification.

The template DNA, pRD05, was alkali denatured, annealed with universal and reverse primers attached to the Autoread Sequencing Kit, and subjected to elongation reaction. The reaction products were analyzed by a sequencer to reveal about 400 bp nucleotide sequences, respectively. Based on these results, FITC labeled sequencing primers described below and called RCE1-01 to 06 were prepared and reacted with pRD05 to further proceed with the sequencing. Consequently, the whole nucleotide sequence of

the insert fragment of pRD05 was determined. The determined nucleotide sequence was translated into an amino acid sequence and one reading frame coincided with a portion of the partial amino acid sequence of endoglucanase RCE I described in Example B1. Thus, the insert DNA contained in the plasmid pRD05 was used as a probe for subsequent screening.

RCE-01: 5'-CAATGTC'TCCCTCTGGAAGCAG-3' (23mer) (SEQ ID NO:46)

RCE-02: 5'-TGCCCTTAGTGACAGCAATGCCC-3' (23mer) (SEQ ID NO:47)

RCE-03: 5'-CTTCCTTCCGCACTCCAAGCTGG-3' (23mer) (SEQ ID NO:48)

RCE-04: 5'-CCAGCTTGGAGTGCGGAAGGAAG-3' (23mer) (SEQ ID NO:49)

RCE-05: 5'-TCTACTAAGGGCAGTGACACCATC-3' (23mer) (SEQ ID NO:50)

RCE-06: 5'-CAGAGGGAAGACATTGAGAGTAG-3' (23mer) (SEQ ID NO:51)

EXAMPLE B4: Preparation of genomic DNA library (Sau3AI library)

The *Rhizopus oryzae* genome DNA was digested with Sau3AI and subjected to 0.8% agarose gel electrophoresis using Agarose LE (Nakara Tesk Japan). After confirming that the genomic DNA was restrictedly digested in the range of 9 to 23 kbp, this DNA fragment was extracted and purified according to conventional methods. This DNA fragment was ligated into a phage vector, Lambda DASH II vector (Stratagene). After ethanol precipitation, the vector was dissolved in TE buffer and entirely packaged into the lambda head by using Giga Pack II Packaging Kit (Stratagene). Then, *E. coli* XL1-Blue strain MRA was infected with the resulting phage. The phage library (5×10^4) obtained by this method was used to clone the target gene.

EXAMPLE B5: Cloning of RCE I gene

(1) Screening by plaque hybridization

First, the plasmid pRD05 obtained in Example B3 was cleaved with BamHI and then subjected to 0.8% agarose gel electrophoresis to recover about 800 bp DNA fragments, which were in turn labeled by ECL Direct DNA/RNA labeling detection system (Amersham).

Then, the DNA genomic library (Sau3AI library) obtained according to Example B4 was transferred to a nylon membrane (Hybond N+ Nylon Transfer Membrane, Amersham). The DNA was fixed with 0.4N sodium hydroxide, washed with 5X SSC (1XSSC, 15 mM

trisodium citrate, 150 mM sodium chloride), and dried to fix the DNA. According to the method of the kit, after prehybridization (42°C) for 1 hour, the labeled probe was added and hybridization (42°C) was carried out for 15 hours. Washing of the label was carried out according to the aforementioned specification attached to the kit. First, washing with 0.4% SDS, 0.5X SSC with 6M urea added at 42°C for 20 minutes were repeated twice and then washing with 2X SSC at room temperature for 5 minutes were carried out twice. After washing the probe, the nylon membrane was immersed in the attached detection solution for 1 minute and then exposed to Fuji Medical X-ray film (Fuji Film) to yield two phage clones.

(2) Preparation of phage DNA

E. coli strain XL1-Blue MRA was infected with the phage and, after 18 hours, phage particles were collected. These particles were treated with proteinase K and phenol according to the method of Grossberger (Grossberger, D., Nucleic Acids Res., 15, 6737 (1987)) and precipitated with ethanol to isolate phage DNAs.

(3) Subcloning of target gene

Two different phage DNAs were digested with plural restriction enzymes and subjected to 0.8% agarose gel electrophoresis. The DNAs were transferred to a nylon membrane by the method of Southern (Southern, E.M., J. Mol. Biol., 98:503-517, 1975) and hybridization was effected in the same manner as in Example B5 (1). As a result, the two phage DNAs showed a common hybridization pattern by digestion with the plural restriction enzymes. When the two phage DNAs were digested with XbaI, they were commonly hybridized with an about 3.5 kbp band. Therefore, this band was recovered and subcloned into the XbaI site of plasmid pUC119. The resulting plasmid was designated as pRCEI-Xba.

EXAMPLE B6: Determination of nucleotide sequence of RCE I gene

The nucleotide sequence was determined by the same method as in Example B3 (3). Thus, the reaction for analysis was carried out using the plasmid pRCEI-Xba obtained in Example B5 as the template DNA and FITC labeled sequencing primers of RCE 01 to 06 as the primers. Based on the results, the following FITC labeled sequencing primers designated as RCEI-07 to 09 were further prepared and each of them was reacted with the

plasmid pRCEI-Xba to analyze and determine the whole nucleotide sequence of the endoglucanase RCE I gene.

RCE-07: 5'-ACAACATTATTTCTTCAAACATG-3' (23mer) (SEQ ID NO:52)

RCE-08: 5'-AAATGCCGCATCAAGTTTATTG-3' (23mer) (SEQ ID NO:53)

RCE-09: 5'-TTCACTTCTACCTCTGTTGCTGG-3' (23mer) (SEQ ID NO:54)

EXAMPLE B7: Expression of RCE I gene

(1) Site-directed mutagenesis of RCE I gene

BglII site was introduced into the sites immediately upstream from the initiation codon and immediately downstream from the termination codon of RCE I gene by site-directed mutagenesis in the following manner.

First, two synthetic oligonucleotides pIN-Bgl and pIC-Bgl as set forth below as primers for mutagenesis were prepared and phosphorylated at 5' end using T4 polynucleotide kinase (Wako Pure Chemical).

Then, site-directed mutagenesis was carried out using Muta-Gene M13 in vitro Mutagenesis Kit (BioRad Laboratory). Thus, *E. coli* strain CJ236 was transformed with plasmid pRCEI-Xba and infected with helper phage M13 KO7 to obtain single-stranded DNAs (ssDNAs). This pRCEI-Xba ssDNA was annealed with the phosphorylated primers pIN-Bgl and pIC-Bgl and subjected to polymerase reaction. The resulting double stranded DNA was introduced into *E. coli* strain JM109 to yield a mutant DNA. This mutagenized plasmid was designated as pRCEI-Bgl.

pIN-Bgl: 5'-GTAATAAACTTCATAGATCTATGTAAAAAGAATG-3' (34mer) (SEQ ID NO:55)

pIC-Bgl: 5'-GGATGAGTATAAAAGATCTTATTTCTTGAAC-3' (32mer) (SEQ ID NO:56)

(2) Expression of RCE I gene in yeast

To express RCE I gene in yeast, the following investigations were done using the host-vector system as described in WO97/00757 specification.

Thus, the plasmid pRCEI-Bgl obtained in Example B7 (1) was digested with BglII and the RCE I gene was recovered. This gene was operably ligated into BamHI site, i.e., downstream from glyceraldehyde-3-phosphate dehydrogenase (GAP) promoter, of plasmid

vector pY2831 to yield a plasmid pYRCEI. This plasmid was used to transform yeast (*Saccharomyces cerevisiae*) strain MS-161 (MATa, trp1, ura3) according to the abovementioned specification to yield a transformant in which the endoglucanase RCE I was capable of expression.

EXAMPLE B8: Evaluation of RCE I expressed in yeast

(1) Cultivation of yeast expressing RCE I

The yeast transformed with the plasmid pYRCEI obtained in Example B7 was cultivated in SD liquid medium (0.67% Yeast nitrogen base w/o amino acids (Difco, 2% glucose) supplemented with 50 µg/ml uracil at 30°C for 24 hours. The seed culture was seeded at a final concentration of 1% in SD liquid medium supplemented with 50 µg/ml uracil and 1% casamino acid and cultivated at 30°C for 36 hours. After cultivation, yeast cells were removed by centrifugation to yield a crude enzyme solution, which was then used in various analyses.

(2) Measurement of molecular weight by SDS-PAGE

The crude enzyme solution obtained in Example B8 (1) was subjected to SDS-PAGE to detect a smear band having a molecular weight of about 100 to 200 kD.

(3) Evaluation of yeast in which RCE I was expressed (CMCase activity)

The crude enzyme solution obtained in Example B8 (1) was used to measure CMCase activity. A cultivation broth of a strain transformed only with the vector DNA into which RCE I gene was not introduced was similarly treated and used as a control.

The results are shown in Table below.

	CMCase (U/ml)
RCE I gene recombinant	1.270
Control	0.000

(4) Evaluation of yeast in which RCE I was expressed (lyocell fuzz removal activity)

The crude enzyme solution obtained in Example B8 (1) was dialyzed and the lyocell fuzz removal activity was measured at 55°C, pH 6 in the same manner as in Example A4. A cultivation broth of a strain transformed only with the vector DNA into

which RCE I gene was not introduced was similarly treated and used as a control.

As a result, no fuzz removal activity was shown in the treatment with 0.5 ml broth/ml of the RCE I gene recombinant strain. Also, no fuzz removal activity was shown in the treatment with 0.5 ml broth/ml of the control reaction solution.

EXAMPLE B9: Expression of mutant endoglucanase RCE I

In Example B8, the endoglucanase RCE I expressed in yeast showed CMCase activity but did not show lyocell fuzz removal activity. Further, the molecular weight measured in Example B8 (2) was higher than expected.

It has been reported by Van Arsdel et al. (Van Arsdel, J.N., 1987, Bio Technology, 5, 60-64) that overglycosylation (excessive addition of sugar chain) sometimes occurs when a foreign protein is expressed in yeast. It was believed that similar phenomenon had occurred in the expression of the endoglucanase RCE I in yeast in Example B8. Accordingly, to express endoglucanase RCE I showing lyocell fuzz removal activity in yeast, a mutant endoglucanase RCE I gene was created wherein amino acids were replaced at asparagine (Asn)-linked glycosylation sites.

(1) Site-directed mutagenesis of RCE I gene

It has been reported by Lehle et al. (Lehle, L. and Bause E., 1984, Biochim. Biophys. Acta., 799, 246-251) that recognition sites of Asn-linked glycosylation, Asn-X-Ser/Thr, are common between yeast and mammalian glycoproteins.

It was believed that endoglucanase RCE I gene has three such sequences and sugar chains bound to asparagine residues at 45th, 90th and 130th positions in the amino acid sequence of SEQ ID NO:1. To express a mutant endoglucanase RCE I which does not have Asn-linked glycosylation site in yeast, site-directed mutagenesis was performed in RCE I gene.

The site-directed mutagenesis was carried out according to the method of Example B7 (1). Thus, three synthetic oligonucleotides pIRI-S47A, pIRI-S92G and pIRI-N130D as set forth below were first prepared as mutagenesis primers and phosphorylated at 5' ends thereof.

Then, *E. coli* strain CJ236 was transformed with plasmid pRCEI-Bgl and a helper phage was used to obtain ssDNA. This ssDNA and primers were annealed and

double-stranded through polymerase reaction using the aforementioned kit and introduced into *E. coli* strain JM109 to yield a mutant DNA, which was designated as pRCEI-NLCD.

pIRI-S47A: 5'-CACTTTCAGAAGCTTTATTGCCAC-3' (24mer) (SEQ ID NO:57)

pIRI-S92G: 5'-GAGCTAGAGCCAGAGTTAGAAG-3' (22mer) (SEQ ID NO:58)

pIRI-N130D: 5'-GAGAACTGACATCGGCCTTACC-3' (22mer) (SEQ ID NO:59)

(2) Expression of mutant endoglucanase RCE I in yeast

The mutant endoglucanase RCE I gene was expressed in yeast according to the method of Example B7 (2). Thus, the plasmid pRCEI-NLCD1 obtained in Example B9 (1) was digested with BglII and a mutant cellulase RCE I gene was recovered. This gene was operably linked to the BamHI site downstream from GAP promoter of plasmid vector pY2831 to yield a plasmid pYI-NLCD. This plasmid was used to transform yeast strain MS-161. Thus, a transformant was obtained in which the mutant endoglucanase RCE I was expressed.

EXAMPLE B10: Evaluation of mutant endoglucanase RCE I expressed in yeast

(1) Cultivation of yeast expressing mutant RCE I

The yeast transformed with the plasmid pYI-NLCD obtained in Example B9 was cultivated under the same conditions as in Example B8 (1) to yield a crude enzyme solution as a cultivation supernatant.

(2) Measurement of molecular weight by SDS-PAGE

The crude enzyme solution obtained in Example B10 (1) was subjected to SDS-PAGE to detect a smear band having a molecular weight of about 40 to 45 kD.

(3) Evaluation of yeast in which mutant RCE I was expressed (CMCase activity)

The crude enzyme solution obtained in Example B10 (1) was used to measure CMCase activity. A cultivation broth of a strain transformed only with the vector DNA into which the mutant RCE I gene was not introduced was similarly treated and used as a control.

The results are shown in Table below.

	CMCase (U/ml)
Mutant RCE I gene recombinant	1.100

Control	0.000
---------	-------

(4) Evaluation of lyocell fuzz removal activity of mutant RCE I expressed in yeast

The crude enzyme solution obtained in Example B10 (1) was dialyzed and the lyocell fuzz removal activity was measured at 55°C, pH 6 in the same manner as in Example A4. As a control, a cultivation broth of a strain transformed only with the vector DNA into which the mutant RCE I gene was not introduced was similarly treated and evaluated.

As a result, 80% of fuzz was removed when treated with 0.1 ml broth/ml of the reaction solution obtained from the mutant RCE I gene recombinant strain. On the other hand, no fuzz was removed when treated with 0.5 ml broth/ml of the control reaction solution.

These results showed that, in order to express RCE I in yeast while exhibiting lyocell fuzz removal activity in yeast, it is necessary to replace amino acids so that RCEI does not have Asn-linked glycosylation site. The amount of protein required to completely remove fuzz was measured by the degree of dyeing after SDS-PAGE. As a result, the mutant endoglucanase RCE I expressed in yeast was almost identical with the endoglucanase RCE I purified by the method shown in Example A1.

(5) Evaluation of lyocell fuzz removal activity at various pHs of mutant RCE I expressed in yeast

The crude enzyme solution obtained in Example B10 (1) was used to measure lyocell fuzz removal activity was measured at pH 4 to 9 in the same manner as in Example A5.

The results are shown in Fig. 2. As seen from the figure, the optimum pH of the mutant RCE I was 7 to 8 and it possessed 80% or more of the activity at the optimum pH over the range of pH 5.2 to 8.6. It is clear that the mutant RCE I expressed in yeast shows similar pH properties as compared with RCE I purified from *Rhizopus oryzae*.

EXAMPLE C1: Search for homologs of RCE I gene in *Rhizopus oryzae*

To search for homologs of endoglucanase RCE I gene in genomic DNA of *Rhizopus oryzae*, analysis was carried out by Southern hybridization.

First, about 10 μ g of genomic DNA of *Rhizopus oryzae* obtained according to Example B2 was digested with plural restriction enzymes (EcoRI, BamHI, HindIII, SacI, XbaI, SalI, etc.) and subjected to 0.8% agarose gel electrophoresis. These materials were transferred to a membrane according to Example B5 (3) and hybridized under the same conditions as in the aforementioned examples. As a result, in addition to the endoglucanase RCE I gene, at least 2 homologous genes were found to be present on the genomic DNA of *Rhizopus oryzae*. These three genes including RCE I gene were detected as a single band respectively, in particular in the hybridization when the genomic DNA was digested with SacI. Accordingly, the gene detected as a band of about 3 kbp (RCE II gene) and the gene detected as a band of about 10 kbp (RCE III gene) were subjected to subsequent cloning.

EXAMPLE C2: Cloning of endoglucanase RCE II gene

(1) Preparation of genomic DNA library (for cloning RCE II gene)

The *Rhizopus oryzae* genome DNA was digested with SacI and subjected to 0.8% agarose gel electrophoresis using Agarose LE to extract and purify DNA fragments of 2 to 4 kbp in size according to conventional methods. This DNA fragment was ligated into a phage vector, Lambda ZAP II vector (Stratagene) and packaged in the same manner as in Example B4. *E. coli* strain XL1-Blue MRF' was infected with the resulting phage. The phage library (1×10^5) obtained by this method was used to clone RCE II gene.

(2) Cloning of RCE II gene

Screening by plaque hybridization was carried out using the library obtained in Example C2 (1) and the long chain probe obtained in Example B3. Hybridization was carried out under the same conditions as in Example B5 to yield three phage clones.

E. coli strain XL1-Blue MRF' was infected with the resulting phage and DNAs were prepared according to the method of Example B5 (2), digested with SacI and subjected to 0.8% agarose gel electrophoresis. The DNAs were transferred to a nylon membrane by the method of Example B5 (3) and hybridized. As a result, a common band having the same size of about 3 kbp as the genomic DNA was detected in the three phage DNAs. This band was recovered and subcloned into the SacI site of plasmid pUC118. The resulting plasmid was designated as pRCEII-Sac.

EXAMPLE C3: Determination of nucleotide sequence of endoglucanase RCE II gene

The nucleotide sequence was determined by the same method as in Example B3 (3). Thus, the reaction for analysis was carried out using the plasmid pRCEII-Sac obtained in Example C2 as the template DNA and the FITC labeled sequencing primers of RCE 03, 04 and 05 prepared in Example B3 (3) as the primers. Based on the results, new FITC labeled sequencing primers were prepared and reacted with the plasmid pRCEII-Sac to further sequence. From the results, the following primers were further prepared to proceed with sequencing. Thus, the nucleotide sequence of RCE II was determined.

RCEII-01: 5'-ACAACATATATTTCTTCGAATATG-3' (23mer) (SEQ ID NO:60)

RCEII-02: 5'-TTTAGCAGCAGAGGCCATTTACAG-3' (23mer) (SEQ ID NO:61)

RCEII-03: 5'-TTTTCTATCCTGATACAGAGATG-3' (23mer) (SEQ ID NO:62)

RCEII-04: 5'-GCGCTCATAAAACGACTACTACC-3' (23mer) (SEQ ID NO:63)

RCEII-05: 5'-TGCCCTTAGTGACAGCAATGTCC-3' (23mer) (SEQ ID NO:64)

EXAMPLE C4: Expression of endoglucanase RCE II gene

(1) Site-directed mutagenesis of RCE II gene

BglIII site was introduced into the sites immediately upstream from the initiation codon and immediately downstream from the termination codon of RCE II gene by site-directed mutagenesis. The method of site-directed mutagenesis followed Example B7 (1).

First, a synthetic oligonucleotide pIIC-Bgl as set forth below as a primer for mutagenesis was newly prepared and phosphorylated at 5' end together with pIN-Bgl previously synthesized in Example B7 (1).

Then, the pRCEII-Sac was brought into single-strand in *E. coli* strain CJ236 and reacted with the phosphorylated primer to yield a mutant DNA. This mutagenized plasmid was designated as pRCEII-Bgl.

pIIC-Bgl: 5'-CAAGAAAATAAGATCTTTTATACTCCTACT-3' (30mer) (SEQ ID NO:65)

(2) Expression of RCE II gene in yeast

Expression of RCE II gene in yeast was carried out according to the method of Example B7 (2). Thus, the plasmid pRCEII-Bgl obtained in Example C4 (1) was digested

with BglII and the endoglucanase RCE II gene was recovered. This gene was operably ligated into BamHI site, i.e., downstream from glyceraldehyde-3-phosphate dehydrogenase (GAP) promoter, of plasmid vector pY2831 to yield a plasmid pYRCEII. This plasmid was used to transform yeast (*Saccharomyces cerevisiae*) strain MS-161 (MATa, trp1, ura3) according to WO97/00757 specification to yield a transformant in which the endoglucanase RCE II was capable of expression.

EXAMPLE C5: Evaluation of endoglucanase RCE II expressed in yeast

(1) Cultivation of yeast expressing RCE II

The yeast transformed with the plasmid pYRCEII obtained in Example C4 was cultivated under the same conditions as in Example B8 (1) to yield a crude enzyme solution as a cultivation supernatant.

(2) Measurement of molecular weight by SDS-PAGE

The crude enzyme solution obtained in Example C4 (1) was subjected to SDS-PAGE to detect a smear band having a molecular weight of about 100 to 200 kD.

(3) Evaluation of yeast in which RCE II was expressed (CMCase activity)

The crude enzyme solution obtained in Example C4 (1) was used to measure CMCase activity. A cultivation broth of a strain transformed only with the vector DNA into which RCE II gene was not introduced was similarly treated and used as a control.

	CMCase (U/ml)
RCE II gene recombinant	0.260
Control	0.000

(4) Evaluation of lyocell fuzz removal activity by mutant RCE II expressed in yeast

The crude enzyme solution obtained in Example C5 (1) was dialyzed and the lyocell fuzz removal activity was measured at 55°C, pH 6 in the same manner as in Example A4. A cultivation broth of a strain transformed only with the vector DNA into which RCE II gene was not introduced was similarly treated and used as a control.

As a result, no fuzz removal activity was shown in the treatment with 0.5 ml broth/ml of the reaction solution of RCE II gene recombinant strain. Also, no fuzz

removal activity was shown in the treatment with 0.5 ml broth/ml of the control reaction solution.

EXAMPLE C6: Expression of mutant endoglucanase RCE II

In Example C4, the endoglucanase RCE II expressed in yeast showed CMCase activity but did not show lyocell fuzz removal activity. Further, the molecular weight measured in Example C4 (2) was higher than expected. It was believed that these results were due to the excessive addition of Asn-linked glycosylation, like the case of RCE I. Accordingly, to express endoglucanase RCE II showing lyocell fuzz removal activity in yeast, a mutant endoglucanase RCE II gene was created wherein amino acids were replaced at asparagine-linked (Asn-type) glycosylation sites.

(1) Site-directed mutagenesis of RCE II gene

It was believed that RCE II gene has five recognition sites of Asn-linked glycosylation, Asn-X-Ser/Thr sequence, and sugar chains bound to asparagine residues at 45th, 92nd, 119th, 122nd and 158th positions in the amino acid sequence of SEQ ID NO:3. To express a mutant endoglucanase RCE II which does not have Asn-linked glycosylation in yeast, site-directed mutagenesis was performed in RCE II gene.

The site-directed mutagenesis was carried out according to the method of Example B7 (1). Thus, four synthetic oligonucleotides pIRII-S47A, pIRII-N92Q, pIRII-S121L:N122D and pIRII-N158D as set forth below were first prepared as mutagenesis primers and phosphorylated at 5' ends thereof.

Then, *E. coli* strain CJ236 was transformed with plasmid pRCEII-Bgl and a helper phage was used to obtain ssDNA. This ssDNA and primers were annealed and double-stranded through polymerase reaction using the aforementioned kit and introduced into *E. coli* strain JM109 to yield a mutant DNA, which was designated as pRCEII-AQLDD.

pIRII-S47A: 5'-AACGGCAATAAGGCCTCTGAATGTAGC-3' (27mer) (SEQ ID NO:66)

pIRII-N92Q: 5'-GAAAGCAATGGCCAGAAAACCTTCTGAAAG-3' (29mer) (SEQ ID NO:67)

pIRII-S121L:N122D: 5'-GCTTCAAACCTCTCTAGACTCTAGCGGC-3' (27mer) (SEQ ID NO:68)

pIRII-N158D: 5'-CGGTAAGGCCGACGTCACTTCTCC-3' (24mer) (SEQ ID NO:69)

(2) Expression of mutant endoglucanase RCE II in yeast

The mutant endoglucanase RCE II gene was expressed in yeast according to the method of Example B7 (2). Thus, the plasmid pRCEII-AQLDD1 obtained in Example C6 (1) was digested with BglII and a mutant endoglucanase RCE II gene was recovered. This gene was operably linked to the BamHI site downstream from GAP promoter of plasmid vector pY2831 to yield a plasmid pYII-AQLDD. This plasmid was used to transform yeast strain MS-161. Thus, a transformant was obtained in which the mutant endoglucanase RCE II was expressed.

EXAMPLE C7: Evaluation of mutant endoglucanase RCE II expressed in yeast

(1) Cultivation of yeast expressing mutant RCE II

The yeast transformed with the plasmid pYII-AQLDD obtained in Example C6 was cultivated under the same conditions as in Example B8 (1) to yield a crude enzyme solution as a cultivation supernatant.

(2) Measurement of molecular weight by SDS-PAGE

The crude enzyme solution obtained in Example C7 (1) was subjected to SDS-PAGE to detect a smear band having a molecular weight of about 45 kD.

(3) Evaluation of mutant RCE II expressed in yeast (CMCase activity)

The crude enzyme solution obtained in Example C7 (1) was used to measure CMCase activity. A cultivation broth of a strain transformed only with the vector DNA into which the mutant RCE II gene was not introduced was similarly treated and used as a control.

	CMCase (U/ml)
Mutant RCE II gene recombinant	0.210
Control	0.000

(4) Evaluation of lyocell fuzz removal activity by mutant RCE II expressed in yeast

The crude enzyme solution obtained in Example C7 (1) was used to measure the lyocell fuzz removal activity at 55°C, pH 6 in the same manner as in Example A4. A

cultivation broth of a strain transformed only with the vector DNA into which the mutant RCE II gene was not introduced was similarly treated and used as a control.

As a result, 60% of fuzz was removed when treated with 0.2 ml broth/ml of the reaction solution of the mutant RCE II gene recombinant strain. On the other hand, no fuzz was removed when treated with 0.5 ml broth/ml of the control reaction solution.

From the above, it was shown that, in order to express RCE II exhibiting lyocell fuzz removal activity in yeast, it is necessary to replace amino acids so that RCEII does not have Asn-linked glycosylation site, as in the case of RCE I. Further, the amount of protein required to completely remove fuzz was measured by the degree of dyeing after SDS-PAGE. As a result, the mutant endoglucanase RCE II expressed in yeast was almost identical with the endoglucanase RCE I purified by the method shown in Example A1.

EXAMPLE C8: Cloning of endoglucanase RCE III gene

(1) Preparation of genomic DNA library (for cloning RCE III gene)

The *Rhizopus oryzae* genome DNA was digested with SacI and subjected to 0.8% agarose gel electrophoresis using Agarose LE to extract and purify DNA fragments of about 10 kbp in size according to conventional methods. This DNA fragment was ligated into Lambda DASH II vector and packaged in the same manner as in Example B4. *E. coli* strain XL1-Blue MRA was infected with the resulting phage. The phage library (1×10^5) obtained by this method was used to clone RCE III gene.

(2) Cloning of RCE III gene

Screening by plaque hybridization was carried out using the library obtained in Example C8 (1) and the long chain probe obtained in Example B3. Hybridization was carried out under the same conditions as in Example B5 to yield two phage clones.

E. coli strain XL1-Blue MRA was infected with the resulting phage and DNAs were prepared according to the method of Example B5 (2). They were digested with plural restriction enzymes and subjected to 0.8% agarose gel electrophoresis. The DNAs were transferred to a nylon membrane according to the method of Example B5 (3) and hybridized. As a result, a common band having the same size as the genomic DNA was detected in the two phage DNAs. In particular, a single band of about 10 kbp or about 2 kbp in size was found in SacI or BamHI cleavage, respectively. Accordingly, the band of

about 2 kbp obtained by BamHI cleavage was recovered and subcloned into the BamHI site of plasmid pUC118. The resulting plasmid was designated as pRCEIII-Bam.

EXAMPLE C9: Determination of nucleotide sequence of endoglucanase RCE III gene

The nucleotide sequence was determined in the same manner as in Example B3 (3). Thus, the reaction for analysis was carried out using the plasmid pRCEIII-Bam obtained in Example C8 as the template DNA and the reverse primer attached to the kit and FITC labeled sequencing primer RCE-06 as the primers. Based on the results, new FITC labeled sequencing primers were prepared and reacted with the plasmid pRCEIII-Bam to further sequence. By further repeating this procedure, the nucleotide sequence of RCE III was determined. The prepared FITC sequencing primers were as follows.

RCEIII-01: 5'-TACAGGAGCCAAACAGGGGAGGTG-3' (23mer) (SEQ ID NO:70)

RCEIII-02: 5'-TTCACAGCAGGTAGGTCCATTCC-3' (23mer) (SEQ ID NO:71)

RCEIII-03: 5'-CCTACGGTTTCGCCGCTGCTTCC-3' (23mer) (SEQ ID NO:72)

RCEIII-04: 5'-TAGATACCAACACCACCACCGGG-3' (23mer) (SEQ ID NO:73)

RCEIII-05: 5'-TGAAGTTCCTTACCATTCGCTCC-3' (23mer) (SEQ ID NO:74)

RCEIII-06: 5'-TGGTGAAACCACTCGCTACTGGG-3' (23mer) (SEQ ID NO:75)

RCEIII-07: 5'-TTCGCTCTGACTGTTCTAACC-3' (23mer) (SEQ ID NO:76)

RCEIII-08: 5'-AATAGAGTTACTCTATACGATAG-3' (23mer) (SEQ ID NO:77)

RCEIII-09: 5'-CACCACCAGAGACAGCGGAGTAG-3' (23mer) (SEQ ID NO:78)

RCEIII-10: 5'-TGCGTTGATTATCCTGACAATCC-3' (23mer) (SEQ ID NO:79)

EXAMPLE C10: Expression of endoglucanase RCE III gene

(1) Site-directed mutagenesis of RCE III gene

BamHI site was introduced into the sites immediately upstream from the initiation codon and immediately downstream from the termination codon of RCE III gene by PCR method in the following manner. First, synthetic oligonucleotides pIIC-Bam1 and pIIC-Bam2 as set forth below as primers for mutagenesis were newly prepared. PCR was carried out using the plasmid pRCEIII-Bam previously obtained in Example C8 as a template, pIIC-Bam1 and pIIC-Bam2 to yield a mutant DNA. This mutant DNA was digested with BamHI and the resulting DNA fragments were recovered and subcloned into BamHI site of the plasmid pUC118. The resulting mutagenized plasmid was designated as

pRCEIII-Bam2.

pIII-C-Bam1: 5'-GCGGATCCATGAAGTTCCTTACCATTGCC -3' (29mer) (SEQ ID NO:80)

pIII-C-Bam2: 5'-GCGGATCCTTATTTTCTTGAACAGCCAGA -3' (29mer) (SEQ ID NO:81)

It was believed that RCE III gene had four recognition sites of Asn-linked glycosylation, Asn-X-Ser/Thr sequence, and sugar chains bound to asparagine residues at 44th, 49th, 121st and 171st positions in the amino acid sequence of SEQ ID NO:5. Accordingly, to express while showing the lyocell fuzz removal activity in yeast, two mutant RCE III genes were prepared, that is, one in which the amino acid at 44th Asn-linked glycosylation site was replaced so that the site was not glycosylated, and the other one in which both the amino acids at 44th and 121st Asn-linked glycosylation sites were replaced so that the sites were not glycosylated.

The site-directed mutagenesis was carried out according to the method of Example B7 (1). Thus, two synthetic oligonucleotides pIRIII-N44D and pIRIII-N121K as set forth below were first prepared as mutagenesis primers and phosphorylated at 5' ends thereof. Then, *E. coli* strain CJ236 was transformed with the plasmid pRCEIII-Bam2 and a helper phage was used to obtain ssDNAs. These ssDNA and primers were annealed and double-stranded through polymerase reaction using the aforementioned kit and introduced into *E. coli* strain JM109 to yield mutant DNAs. The mutagenized plasmid in which only the 44th amino acid had been replaced was designated as pRCEIII-D, and the mutagenized plasmid in which both the 44th and 121st amino acids had been replaced was designated as pRCEIII-DK.

pIRIII-N44D: 5'-GTGGAGGTGAGATCTTCATTGGGAAC-3' (26mer) (SEQ ID NO:82)

pIRIII-N121K: 5'-CAGCGGAGTACTTTGTAGAAGCAG-3' (24mer) (SEQ ID NO:83)

(2) Expression of mutant endoglucanase RCE III in yeast

The mutant RCE III gene was expressed in yeast according to the method of Example B7 (2). Thus, the two plasmids pRCEIII-D and pRCEIII-DK obtained in (1) above were digested with BamHI and mutant RCE III genes were recovered. These genes were operably linked to the BamHI site downstream from GAP promoter of plasmid vector

pY2831 to yield two plasmids pYIII-D and pYIII-DK. These plasmids were used to transform yeast strain MS-161. Thus, transformants were obtained in which the mutant endoglucanase RCE III was expressed.

EXAMPLE C11: Evaluation of mutant endoglucanase RCE III expressed in yeast

(1) Cultivation of yeast expressing mutant RCE III

The yeast transformed with each of the two plasmids pYIII-D and pYIII-DK obtained in Example C10 was cultivated under the same conditions as in Example B8 (1) to yield a crude enzyme solution as a cultivation supernatant.

(2) Evaluation of mutant RCE III expressed in yeast (CMCase activity)

The crude enzyme solution of the yeast transformed with pYIII-DK which was obtained in Example C11 (1) was used to measure CMCase activity. A cultivation broth of a strain transformed only with the vector DNA into which the mutant RCE III gene was not introduced was similarly treated and used as a control.

	CMCase (U/ml)
Mutant RCE III gene recombinant	0.472
Control	0.000

(3) Evaluation of lyocell fuzz removal activity by mutant RCE III expressed in yeast

The two crude enzyme solutions of yeasts transformed with pYIII-D and pYIII-DK which were obtained in Example C11 (1) were dialyzed and then used to measure the lyocell fuzz removal activity at 55°C, pH 6 in the same manner as in Example A4. A cultivation broth of a strain transformed only with the vector DNA into which the mutant RCE III gene was not introduced was similarly treated and used as a control.

As a result, 60% of fuzz was removed by the treatment with 0.2 ml broth/ml of the reaction solution of the mutant RCE III gene recombinant strain (pYIII-D transformant), while 80% of fuzz was removed by the treatment with 0.2 ml broth/ml of the reaction solution of the mutant RCE III gene recombinant strain (pYIII-DK transformant). On the other hand, no fuzz was removed when treated with 0.5 ml broth/ml of the control reaction solution. These results suggested even those in which only amino acid(s) at the nearest

Asn-linked glycosylation site(s) from the cellulose binding domain was/were replaced could exhibit lyocell fuzz removal activity.

EXAMPLE D1: Expression of endoglucanase RCE I gene in *Humicola insolens* (I)

(1) Site-directed mutagenesis of RCE I gene

Mutagenesis of the sequence immediately upstream from the initiation codon of RCE I gene was conducted using PCR method so as to be suitable for expression in *Humicola insolens*. First, a synthetic oligonucleotide pRIN-Bgl as set forth below was newly prepared as a primer for mutagenesis. The PCR was effected using the plasmid pRCEI-Bgl previously obtained in Example B7 (1) as a template, pRIN-Bgl and the synthetic oligonucleotide pIC-Bgl obtained in Example B7 (1), and the amplified fragment of about 1 kB was subcloned into pT7 Blue-T vector. The resulting mutagenized plasmid was designated as pHRCEI-Bgl-11.

The sequence of the oligonucleotide primer prepared upon the mutagenesis is shown below.

pRIN-Bgl: 5'-GGGAGATCTTGGGACAAGATGAAGTTTATTACTATTG-3' (37mer)
(SEQ ID NO:84)

(2) Preparation of plasmid pJRID01

a) Preparation of plasmid pM21-m-A1:

The expression vector pJRID15 of RCE I gene in *Humicola insolens* was constructed in the following manner. First, plasmid pM21 obtained according to WO98/03667 was subjected to site-directed mutagenesis using a synthetic oligonucleotide pMN-Bam. The resulting mutagenized plasmid was designated as pM21-m-A1.

The sequence of the oligonucleotide primer prepared upon mutagenesis is shown below.

pMN-Bam:

5'-GGTCAAACAAGTCTGTGCGGATCCTGGGACAAGATGGCCAAGTCTTCCTTAC
-3' (53mer) (SEQ ID NO:85)

b) Preparation of pJD01:

First, plasmid pM21-m-A1 was digested with HindIII and BamHI and DNA fragment of about 1 kbp was recovered. Then, plasmid pMKD01 obtained according to

WO98/03667 was digested with HindIII and BamHI and DNA fragment of about 7 kbp was recovered. Finally, these DNA fragments were ligated and the resulting plasmid was designated as pJD01.

c) Preparation of plasmid pJRID01:

Plasmid pJD01 was digested with BamHI and then dephosphorylated with alkaline phosphatase (Takara Shuzo). Then, the plasmid pHRCEI-Bgl-11 obtained in (1) above was digested with BamHI and DNA fragment of about 1 kbp was recovered. And, these DNAs were operably linked and the resulting plasmid was designated as pJRID01.

(3) Transformation of *Humicola insolens* with plasmid pJRID01

According to the method described in WO98/03667, *Humicola insolens* MN200-1 was transformed with plasmid pJRID01 and 50 strains showing hygromycin resistance were selected.

EXAMPLE D2: Expression of endoglucanase RCE I gene in *Humicola insolens* (II)

(1) Cultivation of transformant with plasmid pJRID01 and evaluation by SDS-PAGE

According to the method described in WO98/03667, 50 transformants with plasmid pJRID01 were cultivated in (N) medium at 37°C for 4 days. The resulting cultivation supernatant was analyzed by SDS-PAGE but no protein band that increased as compared with the recipient strain was detected.

(2) Evaluation by lyocell fuzz removal activity of transformants with plasmid pJRID01

The cultivation supernatant of 50 transformants with plasmid pJRID01 obtained in (1) above was used to measure lyocell fuzz removal activity. The method followed Example A4 and measurements were done at pH 6, 55°C. As a result, any of the transformants only exhibited lyocell fuzz removal activity substantially similar to the untransformed recipient strain.

EXAMPLE D3: Expression of codon optimized endoglucanase RCE I gene in *Humicola insolens* (I)

From the results of Example D2, endoglucanase RCE I gene derived from *Rhizopus oryzae* was scarcely expressed in *Humicola insolens*. It was believed to be due to a large difference in codon usage between genes derived from *Rhizopus* belonging to *Zygomycetotina* and those derived from *Humicola* belonging to *Deuteromycotina*. Fig. 3

shows the codon usage of endoglucanase RCE I gene. RCE I relatively frequently uses A and T as the third letter in codons. On the contrary, cellulase gene NCE 1 (as described in Japanese Patent Application Laying Open No. 8-56663), NCE 2 (as described in Japanese Patent Application Laying Open No. 8-126492) and NCE 4 (as described in WO98/03640) derived from *Humicola* frequently use G and C as the third letter in codons. Accordingly, it was believed that, in order to express RCE I gene derived from *Rhizopus* in *Humicola*, it was necessary to optimize the codon usage to *Humicola*, more particularly to replace A and T, when used as the third letter in codons, with G and C without changing amino acids encoded thereby. Further, it was believed that, in order to improve stability of mRNA, transcription product of a target gene, it was necessary to not only change the third letters in codons to G and C but also to select such a sequence that does not contain intron recognition sequence, in more particular, such DNA sequences as GTAGN, GTATN, GTAAN, GTACGN, GTGTN, GCACGN and GTTCGN. Thus, codon optimized endoglucanase RCE I gene satisfying the above conditions was designed and fully synthesized as mentioned hereinafter.

(1) Full synthesis of codon optimized endoglucanase RCE I gene

a) Preparation of plasmid p12-BI:

First, two synthetic oligonucleotides having the following sequences were prepared.

RCE I-01: 5'-GGGGGATCCTGGGACAAGATGAAGTTCATCACTATCGCCTCCT
CCGCCCTCCTTGCCCTCGCCCTTGGCACTGAGATGGCCTCCGCCGCTGAGTGCTC
CAAGCTCTACGGCCAGTGGCGGCGAAAGAACTGG-3' (132mer) (SEQ ID NO:86)

RCE I-02: 5'-GGCCGACTCGCTCGACTTGTTCCTCCGAGGAGCCGCTCGGCAG
GCACTGGCTGTAGTAGTCATTCGAGACCTTGCAGGTCGAGCCGCTCTCGCAGCA
GGTGGGGCCGTTCAGTTCTTCCGCCGCACTGGCCGTAG-3' (136mer) (SEQ ID
NO:87)

Then, these oligonucleotides were used to carry out PCR reaction. LA PCR kit (Takara Shuzo) was used in the PCR reaction. dNTP and buffer were added to RCE I-01 and RCE I-02, each 1 μ M, incubated at 94°C for 10 minutes, and ice cooled for 5 minutes. Thereafter, LA Taq polymerase was added and the cycle reaction of 94°C for 30 seconds,

55 °C for 30 seconds and 72°C for 1 minute and 45 seconds was repeated 20 times, followed by incubation at 72°C for 10 minutes. The amplified DNA of about 200 bp was subcloned into pT7 Bleu T-vector according to the method described in Example B3. The resulting plasmid was designated as p12-BI.

b) Preparation of plasmid p123-6:

First, a synthetic oligonucleotide having the following sequence was prepared.

RCE I-P335-Xho-C: 5'-GGGCTCGAGTTGGACGGAGTCGAAGCCTTGGCGACG
GTCGTGGTCTTCTTGGCGGGAGCGGTCGTAGTCTTCTTGAGCGGCGGTCTGT
GTCTTCTTGTGGGCAGCGGTCTTCTTGTGGGCCGACTCGCTCGACTTGT
TTCCC-3' (150mer) (SEQ ID NO:88)

Then, PCR reaction was carried out according to the method of Example D3 (1) a). The template DNA used was 1 µg of plasmid p12-BI and the primers used were RCE I-01 and RCE I-P335-Xho-C, each 1 µM. The PCR reaction was carried out under the same conditions as in Example D3 (1) a) to amplify DNA of about 300 bp. The DNA of about 300 bp was subcloned into pT7 Bleu T-vector and the resulting plasmid was designated as p123-6.

c) Preparation of plasmid p34-6:

First, two synthetic oligonucleotides having the following sequences were prepared.

RCE I-03: 5'-GGAACAAGTCGAGCGAGTCGGCCCAAGAAGACCACGAC
CGCTGCCCACAAGAAGACCACGACCGCCGCTCACAGAAGACTACGACCGCTC
CCGCCAAGAAGACCACGACCGTCGCCAAGGCTTCGACTCCGTCCAACGAGC
AGCTCGTCCTC-3' (158mer) (SEQ ID NO:89)

RCE I-04: 5'-GTCCTTGTTGCAGGACTTGACAGGCGAGCTGACGTTAGCCTT
GCCGGGCCACGAGCACGAAGCCTTGACAGAGTCCAGTAGCGGGTAGTGACGC
CGTTGCCGCTAGCGCCACCGCTGACAGCGCTGTACTTCCCGAGGACGAGCTGC
TCGAGTTGGAC-3' (160mer) (SEQ ID NO:90)

Then, these oligonucleotides were used to carry out PCR reaction. According to the method of Example D3 (1) a), dNTP and buffer were added to RCE I-03 and RCE I-04, each 1 µM, and the reaction was carried out under the same conditions. The amplified

DNA of about 300 bp was subcloned into pT7 Bleu T-vector and the resulting plasmid was designated as p34-6.

d) Preparation of plasmid p3456-18:

First, two synthetic oligonucleotides having the following sequences were prepared.

RCE I-P34-6-Nco-C: 5'-AGCCCATGGCTGGTTGTCGTTGCACATGTAGGAGTT
GCCGCCGTTGCAGCCGGAAGTGGGCGTTGGAGTCGCTAAGAGCGGTGACGCCGTC
CTTGTTGCAGGACTTGACAGGCGAGCTGAC-3' (120mer) (SEQ ID NO:91)

RCE I-P34-6-Sac-C: 5'-GGTGAAGCTCGAAGCAGGAGCAGCACCAGCGGCTCT
CGCCACCGCCGCTAATGGCAGCGGCAGCGAAACCGTAAGCAAGGTTGTCGTTGA
CAGCCCATGGCTGGTTGTCGTTGCACATG-3' (118mer) (SEQ ID NO:92)

Then, PCR reaction was carried out according to the method of Example D3 (1) a). The template DNA used was 1 µg of plasmid p34-6 and the primers used were RCE I-03 and RCE I-P34-6-Nco-C, each 1 µM. The PCR reaction was carried out under the same conditions as in Example D3 (1) a) to amplify DNA of about 400 bp. The DNA of about 400 bp was recovered by using the aforementioned Sephaglas BandPrep kit and the PCR reaction was further carried out using this DNA fragment as a template.

Thus, using about 20 ng of the previously recovered DNA fragment of about 400 bp as a template DNA and 1 µM each of RCE I-03 and RCE I-P34-6-Sac-C as primers, the PCR reaction was carried out under the same conditions as in Example D3 (1) a) to amplify DNA of about 500 bp. The amplified DNA of about 500 bp was subcloned into pT7 Bleu T-vector and the resulting plasmid was designated as p3456-18.

e) Preparation of plasmid p78-2:

First, two synthetic oligonucleotides having the following sequences were prepared.

RCE I-07: 5'-GTGCCCACCTTCGATCTCCAGATGCCGCGCGGCGGCTCGGCA
TCTTCAACGGATGCTCGTCCCAAGTGGGGCGCTCCCAACGACGGCTGGGGCTCGC
GCTACGGCGGCATCAGCTCCGCCAGCGACTGCTCGTCCCTCCCAAGCGCCCTCC
AGGC-3' (154mer) (SEQ ID NO:93)

RCE I-08: 5'-GGGGGGATCCTGCGTTACTTGCGCGAGCATCCGGTCTTAGC

GGTGATCTCCTTGGGGCAGGTGACCTCCTTGTAGGTCATGGACGGGTTGTCGGCG
TTCTTGAACCAAGTTGAAGCGCCACTTGCAGCCGGCCTGGAGGGCGCTGGGGAG
GGAC-3' (154mer) (SEQ ID NO:94)

Then, these oligonucleotides were used to carry out PCR reaction. According to the method of Example D3 (1) a), dNTP and buffer were added to RCE I-07 and RCE I-08, each 1 μ M, and the reaction was carried out under the same conditions. The amplified DNA of about 300 bp was subcloned into pT7 Bleu T-vector and the resulting plasmid was designated as p78-2.

f) Preparation of plasmid p678-8:

First, two synthetic oligonucleotides having the following sequences were prepared.

RCE I-P78-2-SacN: 5'-GGGGAGCTCACCTTCACCTCCACCAGCGTTGCTGGCA
AGAAGATGGTCGTCCAGGTCACCAACACTGGCGGTGACCTTGGCAGCTCGACCG
GTGCCCCACTTCGATCTCCAGATGCCC-3' (117mer) (SEQ ID NO:95)

RCE I-H-C: 5'-GGGGGGATCCTGCGTTTACTTGCGCGAGCATC-3' (32mer) (SEQ ID NO:96)

Then, PCR reaction was carried out according to the method of Example D3 (1) a). The template DNA used was 1 μ g of plasmid p78-2 and the primers used were RCE I-P78-2-SacN and RCE I-H-C, each 1 μ M. The PCR reaction was carried out under the same conditions as in Example D3 (1) a) to amplify DNA of about 400 bp. The DNA of about 400 bp was subcloned into pT7 Bleu T-vector and the resulting plasmid was designated as p678-8.

g) Preparation of plasmid p18-:

First, plasmid p3456-18 was digested with XhoI and SacI to recover DNA fragment of about 300 bp. Then, plasmid p678-8 was digested with SacI and KpnI to recover DNA fragment of about 400 bp. These DNA fragments were ligated using DNA ligation kit and the ligation mixture was subjected to agarose gel electrophoresis to recover DNA fragment of about 700 bp. This DNA fragment was ligated to plasmid p123-6, which had been digested with XhoI and KpnI to yield plasmid p18-1.

(2) Analysis of nucleotide sequence of codon optimized endoglucanase RCE I gene

The nucleotide sequence was analyzed in the same manner as in Example B3 (3). Thus, using plasmid p18-1 obtained in Example D3 (1) g) as a template DNA and newly prepared FITC labeled sequencing primers RCE-H01 to H08 having the following sequences as primers, the reaction was carried out for analysis.

As a result, the whole nucleotide sequence of the codon optimized endoglucanase RCE I gene on the plasmid p18-1 could be analyzed. The codon optimized endoglucanase RCE I gene had the nucleotide sequence of SEQ ID NO:13 and the amino acid sequence deduced from this sequence completely coincided with the amino acid sequence of endoglucanase RCE I of SEQ ID NO:1.

RCE-H01: 5'-TCAGCGGTGGCGCTAGCGCAAC-3' (23mer) (SEQ ID NO:97)

RCE-H02: 5'-CTAATGGCAGCGGCAGCGAAACC -3' (23mer) (SEQ ID NO:98)

RCE-H03: 5'-CCGGTGCCCACTTCGATCTCCAG-3' (23mer) (SEQ ID NO:99)

RCE-H04: 5'-TCTTTCCGCCGCACTGTCCGTAG-3' (23mer) (SEQ ID NO:100)

RCE-H05: 5'-ACGACAACCAGCCATGGGCTGTC-3' (23mer) (SEQ ID NO:101)

RCE-H06: 5'-TCTCGAATGACTACTACAGCCAG-3' (23mer) (SEQ ID NO:102)

RCE-H07: 5'-CCCACTGGGACGAGCATCCGTTG-3' (23mer) (SEQ ID NO:103)

RCE-H08: 5'-CGAGCTGCTCGAGTTGGACGGAG-3' (23mer) (SEQ ID NO:104)

(3) Preparation of plasmid pJ14D01

Plasmid pJD01 obtained in Example D1 (1) was digested with BamHI and then dephosphorylated with alkaline phosphatase. Then, the plasmid p18-1 obtained in Example D3 (1) g) was digested with BamHI to recover DNA fragment of about 1 kbp. And, these DNAs were operably ligated and the resulting plasmid was designated as pJ14D01.

(4) Transformation of *Humicola insolens* with plasmid pJ14D01

According to the method described in WO98/03667, *Humicola insolens* MN200-1 was transformed with plasmid pJ14D01 and 50 strains showing hygromycin resistance were selected.

EXAMPLE D4: Expression of codon optimized endoglucanase RCE I gene in *Humicola insolens* (II)

(1) Cultivation of transformant with plasmid pJ14D01 and evaluation by SDS-PAGE

According to the method described in WO98/03667, 50 transformants with plasmid pJI4D01 were cultivated in (N) medium at 37°C for 4 days. The resulting cultivation supernatant was analyzed by SDS-PAGE to detect a protein band of about 40 kD in molecular weight presumed to be endoglucanase RCE I in 5 strains among the transformants with plasmid pJI4D01.

(2) Evaluation by lyocell fuzz removal activity of transformants with plasmid pJI4D01

Among the 5 strains showing the expression of a protein with molecular weight of about 40 kD by SDS-PAGE in (1) above, the cultivation supernatants of two strains (1-18 and 2-15 strains) which showed particularly significant expression were used to measure lyocell fuzz removal activity. The cultivation supernatant of the untransformed recipient strain was used as a control. According to the method of Example A4, the amount of the cultivation supernatant required to completely remove fuzz was measured by lyocell fuzz removal treatment with various cultivation supernatants under the reaction condition of pH 6, 55°C. The results are shown in Table 3 below.

Table 3

Amount of the cultivation supernatant required for lyocell fuzz removal (ml)

<i>Humicola insolens</i> MN200-1 (recipient)	Only 60% of fuzz were removed even by addition of 8.0 ml.
<i>Humicola insolens</i> pJI4D01 (1-18)	2.0
<i>Humicola insolens</i> pJI4D01 (2-15)	0.1

EXAMPLE D5: Expression of codon optimized endoglucanase RCE I gene in *Humicola insolens* (III)

(1) Evaluation by FPLC of transformant with plasmid pJI4D01

Each of the cultivation supernatants of the transformant (2-15 strain) with plasmid pJI4D01 obtained in Example D4 and the recipient strain was subjected to column chromatography using FPLC system (Pharmacia Biotech) (column: RESOURCETM RPC 3

ml, 5 to 60% acetonitrile gradient containing 0.1% TFA). As a result, a novel peak, which was not seen in the recipient strain, was detected in the cultivation supernatant obtained from the transformant (2-15) with plasmid pJI4D01.

(2) Identification of N-terminal amino acid residues of recombinant endoglucanase RCE I

From Examples D4 and D5 above, it was believed that a recombinant endoglucanase RCE I was expressed in a large amount as the result of optimization of codons in endoglucanase RCE I gene. Accordingly, N-terminal amino acid sequence of this protein was determined in order to confirm that the abundantly expressed protein was derived from the codon-optimized endoglucanase RCE I gene.

First, according to Example D5 (1), the transformant (2-15) with plasmid pJI4D01 was subjected to FPLC system to isolate the resulting novel peak. Then, this peak was centrifuged and subjected to SDS-PAGE (using 8% gel). The protein was electrically transferred to PVDF membrane (Millipore) using MULTIFOR II electrophoretic apparatus (Pharmacia), stained with Coomassie Brilliant Blue R-250, decolorized, washed with water and air-dried. Thereafter, the target band (40 kD) was digested out and subjected to Protein Sequencer Model 492 (Perkin Elmer) to determine 16 residues of N-terminal amino acid sequence. The resulting sequence is shown below.

N-terminal amino acid sequence:

Ala-Glu-(Cys)-Ser-Lys-Leu-Tyr-Gly-Gln-(Cys)-Gly-Gly-Lys-Asn-Trp-Asn (16 residues)
(SEQ ID NO:105)

This N-terminal amino acid sequence coincided with the amino acid sequence of endoglucanase RCE I protein deduced from the nucleotide sequence of plasmid pJI4D01.

Therefore, it was confirmed that the recombinant endoglucanase RCE I was expressed in a large amount in *Humicola insolens* as the result of the optimization of codons in the endoglucanase RCE I gene.

EXAMPLE D6: Expression of codon optimized endoglucanase RCE I gene in *Aspergillus niger* (I)

(1) Acquisition of niaD mutant from *Aspergillus niger* strain FERM P-5886

Spores of *Aspergillus niger* strain FERM P-5886 were smeared on the minimal agar medium (0.2% sodium glutamate, 0.1% dipotassium hydrogenphosphate, 0.05%

magnesium sulfate, 0.05% potassium chloride, 0.001% iron sulfate, 3% sucrose, 1.5% agar, pH 5.5) containing 6% chlorate and incubated at 30°C. After cultivation for about 5 days, those forming colonies were taken as chlorate resistant strains. These resistant strains were inoculated in the minimal medium containing glutamate, nitrate or nitrite, respectively, as a single nitrogen source to investigate nitrogen requirements. As a result, there was present chlorate resistant strains which could grow in the minimal medium containing sodium glutamate or nitrite as a single nitrogen source but could not grow in nitrate. These strains were taken as candidates for *niaD* mutant.

With 3 strains among the *niaD* mutant candidates, the nitrate reductase (nitrate reducing enzyme, which is a *niaD* gene product) activity in the cells was measured. These three strains were shaker cultivated in a liquid medium (0.25% sodium glutamate, 0.1% dipotassium hydrogenphosphate, 0.05% magnesium sulfate, 0.05% potassium chloride, 0.001% iron sulfate, 3% sucrose) at 30°C for 60 hours. The resulting wet cells (0.2 g) were suspended in 2 ml of 50 mM sodium phosphate buffer (pH 7.5) and crushed by an ultrasonic homogenizer. After insoluble fractions were removed by centrifugation, the cultivation supernatant was taken as a sample. To 50 µl of the sample solution, 1000 µl of distilled water, 750 µl of 0.2 M sodium phosphate solution (pH 7.5), 100 µl of 0.04 mg/ml FAD, 100 µl of 2 mg/ml NADPH, and 1000 µl of 22.5 mg/ml sodium nitrate were added, followed by reacting at 37°C. After the reaction, 500 µl of 1% sulfanilamide (dissolved by 3N hydrochloric acid) and 500 µl of 0.02% N-1-naphthyl-ethylenediamine were added to the sample for color formation and A540 was measured to detect the nitrate reductase activity. However, no nitrate reductase activity was detected in these three strains. Therefore, it was concluded that these three strains were *niaD* mutant strains and one of them was designated as NIA5292 strain, which was subjected to subsequent experiments.

(2) Acquisition of *niaD* gene from *Aspergillus niger* strain FERM P-5886

a) Preparation of probe:

Aspergillus niger strain NRRL4337 was cultivated in YPD liquid medium (1% yeast extract, 2% polypeptone, 2% glucose). DNA was amplified by PCR method using the total DNA extracted from the resulting cells by the known method (Japanese Patent Application Laying Open No. 8-53522) as a template and synthetic DNA primers of SEQ

ID NOs:106 and 107 prepared based on the nucleotide sequence of *Aspergillus niger* *niaD* gene described in Unkles, S.E., et al., Gene, 111, 149-155 (1992) as primers. The reaction solution contained 0.5 µg chromosome DNA, 100 pmol each primer and 2.5 U Taq DNA polymerase (Nippon Gene) per 100 µl. The reaction was carried out 25 cycles under the temperature conditions of 94°C for 1 minute, 50°C for 2 minutes and 72°C for 2 minutes to specifically amplify DNA fragment of about 800 bp. The nucleotide sequence of this DNA fragment was determined and completely (100%) coincided with the nucleotide sequence of *Aspergillus niger* *niaD* gene already reported. Thus, it was clarified that this DNA fragment was derived from *niaD* gene. Accordingly, this DNA fragment of about 800 bp was taken as a probe for use.

NIA-CN: 5'- GACTGACCGGTGTTTCATCC-3' (19mer) (SEQ ID NO:106)

NIA-CC: 5'- CTCGGTTGTCATAGATGTGG-3' (20mer) (SEQ ID NO:107)

b) Southern analysis of chromosome DNA of *Aspergillus niger*:

Aspergillus niger strain FERM P-5886 was cultured in YPD liquid medium (1% yeast extract, 2% polypeptone, 2% glucose). Total DNA extracted from the resulting cells by the known method (Japanese Patent Application Laying Open No. 8-53522) was completely digested with restriction enzymes (HindIII, EcoRI, BamHI, SacI, SalI, XbaI), fractionated by agarose gel electrophoresis, and blotted on nylon membrane (Hybond-N+, Amersham) according to the method described in Molecular Cloning (Cold Spring Harbour, 1982). Southern hybridization was effected to the nylon membrane using the aforementioned 800 bp DNA fragment as a probe. For labeling probes and detecting signals, Ecl DirectI DNA Labeling-Detection System (Amersham) was used under the conditions following the manual attached. As a result, signals were detected at positions of about 6.5 kbp upon digestion with SalI.

c) Isolation of *niaD* gene:

Total DNA of *Aspergillus niger* strain FERM P-5886 was partially cleaved with restriction enzyme MboI, and fractionated by agarose gel electrophoresis. DNA fragments near 9-23 kbp were extracted and recovered by conventional methods. The recovered DNA fragment was ligated into BamHI site of λ DASHII and packaged by GIGAPACK II Gold (Stratagene). *E. coli* was infected with the phage to prepare a library.

Plaque hybridization was carried out using the aforementioned 800 bp DNA fragment as a probe and Ecl DirectI DNA Labeling-Detection System (Amersham), to obtain positive clones. The resulting positive clones were subjected to secondary screening to purify the positive clones.

Phage DNA was prepared from the positive clones to confirm the insertion of about 6.5 kbp *Sall* fragment. This DNA was subjected to Southern analysis to find a smaller DNA fragment of about 4.8 kbp *SacI* fragment. The restriction enzyme map of this fragment was made. Further, this *SacI* fragment was subcloned into plasmid pUC118. The resulting plasmid was designated as *pniaD-Sac*. This *SacI* fragment was further digested with suitable restriction enzyme(s) and then subcloned into pUC118. This was used as a template to determine the nucleotide sequence and the position of *niaD* gene in the isolated DNA fragment was identified.

(3) Transformation of *Aspergillus niger* strain NIA5292

Aspergillus niger strain NIA5292 was shaker cultivated in a liquid medium (2% soluble starch, 1% polypeptone, 0.2% yeast extract, 0.5% sodium dihydrogenphosphate, 0.05% magnesium sulfate) at 28°C for 24 hours. Cells were collected by a glass filter, suspended into an enzyme solution (1 mg/ml β -glucuronidase (Sigma), 5 mg/ml Novozyme 234 (Novo Nordisk), 10 mM sodium phosphate (pH 5.8), 0.8 M potassium chloride), and gently heated at 30°C for 1.5 hours. Protoplasts were filtered through a glass filter and the passed fraction was centrifuged to collect cells, which were washed twice with STC buffer (10 mM Tris (pH 7.5), 10 mM potassium chloride, 1.2 M sorbitol) and suspended into STC buffer. Subsequently, the protoplast and plasmid DNA were mixed and allowed to stand on ice for 20 minutes. Further, PEG solution (10 mM Tris (pH 7.5), 10 mM potassium chloride, 60% polyethylene glycol 4000) was added and allowed to stand on ice for another 20 minutes to introduce the DNA into the protoplast. The protoplast was washed several times with STC buffer, suspended in Czapek medium (0.2% sodium nitrate, 0.1% dipotassium hydrogenphosphate, 0.05% magnesium sulfate, 0.05% potassium chloride, 0.001% ferric sulfate, 3% sucrose) containing 1.2 M sorbitol and 0.8% agar, layered on Czapek agar medium containing 1.2 M sorbitol and 1.5% agar, and cultivated at 30°C. After cultivation for about 5 days, those forming colonies were selected as transformants.

EXAMPLE D7: Expression of codon optimized endoglucanase RCE I gene in *Aspergillus niger* (II)

(1) Preparation of plasmid pSAEX11

An expression vector having an amylase promoter operable in *Aspergillus niger* was constructed in the following manner.

a) Preparation of plasmid pAMYI:

First, plasmid pAMY obtained according to WO97/00944 was digested with restriction enzymes EcoRI and SalI and the resulting DNA fragment of about 0.75 kb was ligated to pUC119 also digested with EcoRI and SalI. The resulting plasmid was designated as pAMYI.

b) Site-directed mutagenesis of plasmid pAMYI:

BamHI site was introduced into a site immediately upstream from the initiation codon of amylase gene by site-directed mutagenesis. The method of site-directed mutagenesis followed Example B7 (1).

First, a synthetic oligonucleotide pAMBM as set forth below as a primer for mutagenesis was newly prepared and phosphorylated at 5' end. Then, the plasmid pAMYI was brought into single-strand in *E. coli* strain CJ236 and reacted with the phosphorylated primer to yield a mutant DNA. This mutagenized plasmid was designated as pAMY-Bam. pAMBM: 5'-CCCACAGAAGGGATCCATGATGGTCGC -3' (27mer) (SEQ ID NO:108)

c) Preparation of plasmid pSAEX11:

First, plasmid pAMY-Bam was digested with restriction enzymes EcoRI and BamHI and the resulting DNA fragment of about 0.6 kb was recovered. Then, plasmid pDH25 obtained according to Cullen et al. report (Cullen, D., Gene, 57, 21-26, 1987) was digested with EcoRI and BamHI and the resulting DNA fragment of about 4.7 kb was recovered. The both were ligated and the resulting plasmid was designated as pSAEX11.

(2) Preparation of plasmids pANR22 and pANH42

In order to express the endoglucanase RCE I gene derived from *Rhizopus* and the codon optimized endoglucanase RCE I gene prepared by full synthesis in *Aspergillus niger*, expression vectors pANR22 and pANH42 were constructed.

a) Preparation of plasmids pANR21 and pANH41:

First, plasmid pHRCEI-Bgl-11 was digested with restriction enzyme BglII and the resulting DNA fragment of about 1 kb was recovered as the endoglucanase RCE I gene fragment derived from *Rhizopus*. Also, plasmid pJI4D01 was digested with BamHI and the resulting DNA fragment of about 1 kb was recovered as the codon optimized endoglucanase RCE I gene fragment.

Then, plasmid pSAEX11 was digested with BamHI and ligated to each of the BglII fragment of the endoglucanase RCE I gene and the BamHI fragment of the codon optimized endoglucanase RCE I gene. The resulting plasmids were designated as pANR21 and pANH41, respectively.

b) Preparation of plasmids pANR22 and pANH42:

First, plasmids pANR21 and pANH41 were digested with restriction enzyme XbaI. Then, plasmid pniaD-Sac described in Example D6 was digested with restriction enzyme XbaI to yield a fragment of about 4.8 Kbp. This fragment contained from the restriction enzyme XbaI recognition site present immediately after the restriction enzyme SacI recognition site in the upstream region of niaD gene to the restriction enzyme XbaI recognition site derived from pUC118 present immediately after the restriction enzyme SacI recognition site in the downstream region of niaD gene. This 4.8 kbp fragment was inserted into XbaI site of plasmids pANR21 and pANH41. The resulting plasmids were designated as pANR22 and pANH42.

EXAMPLE D8: Expression of codon optimized endoglucanase RCE I gene in *Aspergillus niger* (III)

(1) Transformation of *Aspergillus niger* strain NIA5292 with plasmids pANR22 and pANH42

According to the method described in Example D6, *Aspergillus niger* strain NIA5292 was transformed with plasmids pANR22 and pANH42, as well as the vector only as a control. About 50 strains each of the transformants on Czapek agar medium were cultivated in SMPN liquid medium (3% soluble starch, 0.7% malt extract, 1% polypeptone, 0.3% NaCl) at 28°C for 3 days. After the cultivation supernatant was dialyzed, lyocell fuzz was removed under the reaction condition of pH 6, 55°C according to Example A4 to investigate the degree of fuzz removal. The results are shown in Table 4. The cultivation

broth of the transformant with plasmid pANH42 showed activity in the removal of fuzz from lyocell, while the cultivation broth of strains transformed with the vector only or with plasmid pANR22 showed no lyocell fuzz removal activity.

Table 4
Degree of lyocell fuzz removal

<i>Aspergillus niger</i> (vector only)	No fuzz was removed.
<i>Aspergillus niger</i> pANR22	No fuzz was removed.
<i>Aspergillus niger</i> pANH42	80% of fuzz were removed.

EXAMPLE D9: Expression of codon optimized endoglucanase RCE I gene from which a part of the linker region was deleted in *Humicola insolens*

(1) A part of the linker region in RCE I gene in the plasmid pJI4D01 (from the 331st base G to the 405th base C in SEQ ID NO:13) was deleted using PCR and this plasmid was designated as pJI4D10.

(2) Cultivation of transformant with plasmid pJI4D10 and evaluation by SDS-PAGE

According to the method described in WO98/03667, 30 transformants with plasmid pJI4D10 were cultivated in (N) medium at 37°C for 4 days. The resulting cultivation supernatant was analyzed by SDS-PAGE to detect a protein band of about 30-35 kD in molecular weight presumed to be a deleted RCE I in 5 strains among the transformants with plasmid pJI4D10.

(3) Evaluation of lyocell fuzz removal activity of transformants with plasmid pJI4D10

Among the 5 strains showing the expression of a protein with molecular weight of about 30-35 kD by SDS-PAGE in (2) above, the cultivation supernatant of one strain (3-13 strain) which showed particularly significant expression was used to measure lyocell fuzz removal activity. The cultivation supernatant of 2-15 strain from which a portion of linker region of RCE I was not deleted was used as a control. According to the method of Example A4, the degree of fuzz removal was investigated by lyocell fuzz removal treatment with various cultivation supernatants (each 0.1 ml) under the reaction condition of pH 6,

55°C. The results are shown in Table 5 below.

Table 5

Degree of lyocell fuzz removal

<i>Humicola insolens</i> pJI4D01 (2-15)	Fuzz was removed completely.
<i>Humicola insolens</i> pJI4D10 (3-13)	No fuzz was removed.

EXAMPLE E1: Search for homologs of RCE I gene in *Mucor circinelloides*

To search for homologs of endoglucanase RCE I gene in genomic DNA of *Mucor circinelloides*, analysis was carried out by Southern hybridization.

First, about 10 µg of genomic DNA of *Mucor circinelloides* obtained according to Example B2 was digested with plural restriction enzymes (EcoRI, BamHI, HindIII, SacI, XbaI, Sall, etc.) and subjected to 0.8% agarose gel electrophoresis. These materials were transferred to a membrane according to Example B5 (3) and hybridized using RCE I gene as a probe under the same conditions as in the aforementioned examples. As a result, it was found that at least one homologous gene was present on the genomic DNA of *Mucor circinelloides*. This gene was detected as a single band, particularly in the hybridization when the genomic DNA was digested with EcoRI. Accordingly, the gene detected as a band of about 4.5 kbp was designated as MCE I and subjected to subsequent cloning.

EXAMPLE E2: Cloning of endoglucanase MCE I gene

(1) Preparation of genomic DNA library (for cloning MCE I gene)

The genome DNA of *Mucor circinelloides* was digested with EcoRI and subjected to 0.8% agarose gel electrophoresis using Seakem LE agarose to extract and purify DNA fragments of about 3 to 6.5 kbp in size according to conventional methods. These DNA fragments were ligated into a phage vector, Lambda gt10 vector (Stratagene) and packaged in the same manner as in Example B4. *E. coli* strain NM514 was infected with the resulting phage. The phage library (1×10^8) obtained by this method was used to clone MCE I gene.

(2) Cloning of MCE I gene from genomic DNA

Screening by plaque hybridization was carried out using the library obtained in Example E2 (1) and RCE I gene probe. Hybridization was carried out under the same conditions as in Example B5 to yield 6 phage clones.

E. coli strain NM514 was infected with the resulting phage and DNAs were prepared according to the method of Example B5 (2), digested with EcoRI and subjected to 0.8% agarose gel electrophoresis. The DNAs were transferred to a nylon membrane according to the method of Example B5 (3) and hybridized. As a result, a common band having the same size of about 4.5 kbp as the genomic DNA was detected in the 6 phage DNAs. This band was recovered and subcloned into the EcoRI site of plasmid pUC119. The resulting plasmid was designated as pMCEI-Eco. The nucleotide sequence of this about 4.5 kbp was determined in the same manner as in Example B3 (3). The elucidated nucleotide sequence was translated into an amino acid sequence. A reading frame coincided with the N-terminal amino acid sequence of endoglucanase MCE I as shown in Example B1. However, it was presumed that this sequence contained introns and, therefore, cDNA of MCE I gene was isolated by RT-PCR.

(3) Isolation of cDNA of MCE I gene by RT-PCR and determination of nucleotide sequence

Mucor circinelloides was cultivated in 30 ml of liquid medium (3.0% corn steep liquor, 0.5% yeast extract (Difco), 2.4% potato dextrose broth (Difco), 2% sucrose) at 30 °C for 18 hours and the cells were collected by a glass filter. The resulting cells were lyophilized and finely crushed by a spatula. Total RNA was isolated using Isogen (Wako Pure Chemical Industry). First, 5 ml of Isogen was added to the cell powder, vortexed for 30 seconds and incubated at 50°C for 10 minutes, followed by allowing to stand at room temperature for 5 minutes. Then, 0.8 ml of chloroform was added and vigorously shaken. After centrifugation, the aqueous layer was transferred to another vessel, to which 2 ml of 4 M LiCl was added and mixed, followed by allowing to stand at -70°C for 15 minutes. Thereafter, the material was centrifuged and the supernatant was removed. The precipitate was dissolved in 1.6 ml of water and 1.6 ml of isopropanol was added and mixed, followed by allowing to stand at 4°C for 30 minutes. After centrifugation, the supernatant was removed and the precipitate was washed with 75% ethanol. The precipitate was dissolved in 1.6 ml of water. This solution was precipitated with ethanol and the precipitate was

washed with 75% ethanol, dried and dissolved in 0.4 ml of water to yield total RNA.

Then, mRNA was prepared using mRNA Isolation Kit (Stratagene). First, 10 ml of Elution Buffer was added to 0.2 ml of total RNA prepared above, and 5 ml of oligo dT solution was further added. After removing the supernatant, the oligo dT was washed three times with High Salt Buffer and twice with Low Salt Buffer and then eluted with Elution Buffer heated to 68°C. This solution was precipitated with ethanol and the precipitate was washed with 75% ethanol, dried and dissolved in 15 µl of water to yield mRNA fraction.

Then, cDNA of MCE I gene was prepared from the mRNA by RT-PCR using Takara RNA PCR Kit (AMV) Ver. 2.1. Thus, oligonucleotide primers having the following sequences were prepared as primers for N- and C-terminals deduced from the genomic MCE I gene sequence determined above and only cDNA of MCE I gene was amplified by PCR method using 1 µl of mRNA prepared above as a template.

MCEI-CN: 5'-GCGAATTCATGAAGTTCACCGTTGCTATT-3' (29mer) (SEQ ID NO:109)

MCEI-CC: 5'-GCGAATTCCTTACTTCTTTTCGCAACCTG-3' (28mer) (SEQ ID NO:110)

The RT-PCR reaction was effected under the following conditions. First, the C-terminal primer was added to the reaction mixture and reacted with reverse transcriptase. Then, Taq polymerase (recombinant Taq, Takara Shuzo) and the N-terminal primer were added and the reaction conditions of 94°C for 1 minute, 50°C for 2 minutes and 72°C for 2 minutes were repeated 30 times to amplify. As a result of agarose gel electrophoresis, the amplified fragments were two fragments of about 1.1 kbp and 1.0 kbp. These fragments were subcloned into EcoRI site of pUC118 and the nucleotide sequences of the respective fragments were determined according to the method of Example B3 (3). This nucleotide sequence was compared with the genomic nucleotide sequence to determine introns. As a result of this analysis, it was found that in *Mucor circinelloides*, two endoglucanases were expressed wherein the gene sequences were identical with each other in a portion of N- and C-terminals. Accordingly, the endoglucanases encoded by the shorter (about 1.0 kbp) and longer (about 1.1 kbp) nucleotide sequences were designated as MCE I and MCE II,

respectively.

EXAMPLE E3: Expression of endoglucanase MCE I gene

(1) Site-directed mutagenesis of MCE I gene

The cDNA of MCE I gene prepared by RT-PCR had a mutation. This mutation was restored by site-directed mutagenesis. This MCE I plasmid subcloned into EcoRI site of pUC118 was designated as pMCEI-EcoRI. Further, MCE I gene had one Asn-linked glycosylation site, Asn-X-Ser/Thr sequence, and it was believed that an oligosaccharide chain bound to the asparagine residue at 50th position in the amino acid sequence of SEQ ID NO:7. Since it was believed that lyocell fuzz removal activity would be inhibited by excessive glycosylation in the Asn-linked glycosylation sites like RCE I, a mutant endoglucanase MCE I gene in which the amino acid at the Asn-linked glycosylation site was replaced was created by site-directed mutagenesis.

The site-directed mutagenesis was carried out according to the method of Example B7 (1). Thus, a synthetic oligonucleotide pIMI-S52G as set forth below was prepared as a mutagenesis primer and phosphorylated at 5' end thereof. Then, *E. coli* strain CJ236 was transformed with plasmid pMCEI-EcoRI and a helper phage was used to obtain ssDNA. This ssDNA and primer were annealed and double-stranded through polymerase reaction using the aforementioned kit and introduced into *E. coli* strain JM109 to yield a mutant DNA, which was designated as pMCEI-G.

PIMI-S52G: 5'-CTTGGTGCTGCCAGCGTTACCAG -3' (23mer) (SEQ ID NO:111)

(2) Expression of mutant MCE I gene in yeast

The mutant RCE I gene was expressed in yeast according to the method of Example B7 (2). Thus, the plasmid pMCEI-G obtained in Example E3 (1) was digested with EcoRI and a mutant MCE I gene was recovered. This gene was operably linked to the EcoRI site downstream from glyceraldehyde-3-phosphate dehydrogenase (GAP) promoter of plasmid vector pY2831 to yield a plasmid pYMCEI. This plasmid was used to transform yeast (*Saccharomyces cerevisiae*) strain MS-161 (MATa, trp1, ura3) according to WO97/00757 specification. Thus, a transformant was obtained in which the endoglucanase MCE I could be expressed.

EXAMPLE E4: Evaluation of mutant endoglucanase MCE I expressed in yeast

(1) Cultivation of yeast expressing mutant MCE I

The yeast transformed with the plasmid pYMCEI obtained in Example E3 was cultivated under the same conditions as in Example B8 (1) to yield a crude enzyme solution as a cultivation supernatant.

(2) Measurement of molecular weight by SDS-PAGE

The crude enzyme solution obtained in Example E4 (1) was subjected to SDS-PAGE to detect a smear band having a molecular weight of about 45 kD.

(3) Evaluation of yeast in which mutant MCE I was expressed (CMCase activity)

The crude enzyme solution obtained in Example E4 (1) was used to measure CMCase activity. A cultivation broth of a strain transformed only with the vector DNA into which the mutant MCE I gene was not introduced was similarly treated and used as a control.

	CMCase (U/ml)
Mutant MCE I gene recombinant	0.337
Control	0.000

(4) Purification of mutant MCE I expressed in yeast

An ammonium sulfate solution at a final concentration of 1.5 M was prepared from 500 ml of the crude enzyme solution obtained in Example E4 (1) and applied at a flow rate of 3.0 ml/min to Macro-Prep Methyl HIC Support hydrophobic chromatography (25 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.5 M ammonium sulfate solution. It was then fractionated by eluting at a flow rate of 5.0 ml/min in a stepwise elution method in which the concentration of ammonium sulfate in deionized water was decreased by 0.3 M each from 1.5 M. Among the fractions, the fraction obtained at an ammonium sulfate concentration of 0.6 M was found to have a strong lyocell fuzz removal activity. Therefore, 50 ml of this fraction was isolated. By repeating twice the fractionation by Macro-Prep Methyl HIC Support hydrophobic chromatography, 1000 ml of the cultivation supernatant were treated to provide 100 ml of active fractions.

An ammonium sulfate solution at a final concentration of 1.5 M was prepared from 100 ml of the active fractions and applied to Econo-Pac Methyl HIC Cartridge hydrophobic

chromatography (5 ml in gel volume, BioRad Laboratories) which had been equilibrated with 1.5 M ammonium sulfate solution. Then, 1.5 M ammonium sulfate solution was applied. Deionized water was then applied and 1 ml each and the fractions, which were found to have a strong lyocell fuzz removal activity were pooled, fractionated the eluted fractions. This fraction showed an almost single smear band in SDS-PAGE and had a molecular weight (MW) of about 45 kD. The SDS-PAGE used NPU-12.5L PAGEL (ATTO Japan) and migration and dyeing were carried out according to the specification attached to the gel. Molecular weight standards used were SDS-PAGE molecular weight standard Low range (BioRad Laboratories).

(5) Evaluation of lyocell fuzz removal by purified mutant MCE I (specific activity in the removal of fuzz from lyocell)

The purified enzyme solution of mutant MCE I obtained in Example E4 (4) was used to evaluate lyocell fuzz removal activity under the conditions as set forth below in the same manner as in Example A4. Thus, a knitted fabric of lyocell (Toyoshima Japan, 9 cm x 10 cm, about 2 g in weight) fuzzed by the method of Example A4 was subjected to lyocell fuzz removal treatment under the conditions as set forth below, whereby the protein concentration of mutant MCE I required to completely remove fuzz formed was calculated.

The protein concentrations of mutant MCE I were calculated from the peak area at UV 280 nm of various endoglucanases eluted with a linear gradient from 0% to 80% of acetonitrile concentration in 0.05% TFA (trifluoroacetic acid) at a flow rate of 1.0 ml/min in HPLC analysis using TSK gel TMS-250 column (4.6 mm I.D. x 7.5 cm, Toso Japan). The standard used was a purified NCE4 which was analyzed in HPLC under the same conditions, the protein concentration of which had been preliminarily measured by Protein Assay Kit (BioRad Laboratories). The standard used to measure the protein concentration in the protein assay kit was Albumin Standard (Bovine serum albumin, fraction V, PIERCE).

Test machine: Launder Meter L-12 (Daiei Kagaku Seiki MFG., Japan)

Temperature: 50°C

Time: 60 minutes

Reaction volume: 40 ml

Reaction pH: pH 5 (10 mM acetate buffer)

pH 6 (10 mM acetate buffer)

The treating liquid contained 4 rubber balls (about 16 g each) together with the endoglucanase solution.

The results are as shown in Table 6 below. The mutant endoglucanase MCE I expressed in yeast had an almost identical lyocell fuzz removal activity per enzyme concentration with the endoglucanase MCE I purified by the method as shown in Example A2.

Table 6

Enzyme	pH 5	pH 6
MCE I	0.5 mg/l	0.5 mg/l

(6) Evaluation of lyocell fuzz removal by mutant MCE I expressed in yeast at different pHs (pH profile lyocell fuzz removal activity of MCE I)

The crude MCE I enzyme solution obtained in Example E4 (1) was used to evaluate lyocell fuzz removal activity at a pH of 4 to 10 under the condition of 50°C according to the method of Example A5.

The results are shown in Fig. 2. As seen from the figure, the optimum pH for MCE I was 5-6 and 60% or more of the activity at the optimum pH was maintained in the range of pH 5 to 8. It is apparent that, like MCE I purified from *Mucor circinelloides* in Example A2, the mutant MCE I expressed in yeast is significantly highly active in the alkaline conditions as compared with the purified NCE4.

EXAMPLE F1: Search for homologs of RCE I gene in *Phycomyces nitens*

To search for homologs of endoglucanase RCE I gene in genomic DNA of *Phycomyces nitens*, analysis was carried out by Southern hybridization.

First, about 10 µg of genomic DNA of *Phycomyces nitens* obtained according to Example B2 was digested with plural restriction enzymes (EcoRI, BamHI, HindIII, SacI,

XbaI, SalI, etc.) and subjected to 0.8% agarose gel electrophoresis. These materials were transferred to a membrane according to Example B5 (3) and hybridized using RCE I gene and codon optimized RCE I gene as probes under the same conditions as in the aforementioned examples. As a result, it was found that at least one gene homologous with the codon optimized RCE I gene was present on the genomic DNA of *Phycomyces nitens*.

This gene was detected as a single band, particularly in the hybridization when the genomic DNA was digested with BamHI. Accordingly, the gene detected as a band of about 15 to 19 kbp was designated as PCE I and subjected to subsequent cloning.

EXAMPLE F2: Cloning of endoglucanase PCE I gene

(1) Preparation of genomic DNA library (for cloning PCE I gene)

The genome DNA of *Phycomyces nitens* was digested with BamHI and subjected to 0.8% agarose gel electrophoresis using Seakem LE agarose to extract and purify DNA fragments of about 9 to 23 kbp in size according to conventional methods. These DNA fragments were ligated into a phage vector, Lambda DASH II vector (Stratagene) and packaged in the same manner as in Example B4. *E. coli* strain XL1-Blue MRA was infected with the resulting phage. The phage library (1.6×10^4) obtained by this method was used to clone PCE I gene.

(2) Cloning of PCE I gene from genomic DNA

Screening by plaque hybridization was carried out using the library obtained in Example F2 (1) and codon optimized RCE I gene probe. Hybridization was carried out under the same conditions as in Example B5 to yield 6 phage clones. *E. coli* strain XL1-Blue MRA was infected with the resulting phage and DNAs were prepared according to the method of Example B5 (2), digested with XbaI and subjected to 0.8% agarose gel electrophoresis. The DNAs were transferred to a nylon membrane according to the method of Example B5 (3) and hybridized. As a result, a common band of about 2.3 kbp was detected in the 6 phage DNAs. This band was recovered and subcloned into the XbaI site of plasmid pUC119. The resulting plasmid was designated as pPCEI-Xba. The nucleotide sequence of this about 2.3 kbp was determined in the same manner as in Example B3 (3). The elucidated nucleotide sequence was translated into an amino acid

sequence. A reading frame coincided with the N-terminal amino acid sequence of endoglucanase PCE I as shown in Example B1. However, it was presumed that this sequence contained introns and, therefore, cDNA of PCE I gene was isolated by RT-PCR.

(3) Isolation of cDNA of PCE I gene by RT-PCR and determination of nucleotide sequence

Phycomyces nitens was cultivated in 30 ml of liquid medium (3.0% corn steep liquor, 0.5% yeast extract (Difco), 2.4% potato dextrose broth (Difco), 2% sucrose) at 30°C for 48 hours and the cells were collected by a glass filter. The resulting cells were lyophilized and finely crushed by a spatula. Total RNA was isolated using Isogen (Wako Pure Chemical Industry). First, 5 ml of Isogen was added to the cell powder, vortexed for 30 seconds and incubated at 50°C for 10 minutes, followed by allowing to stand at room temperature for 5 minutes. Then, 0.8 ml of chloroform was added and vigorously shaken. After centrifugation, the aqueous layer was transferred to another vessel, to which 2 ml of 4 M LiCl was added and mixed, followed by allowing to stand at -70°C for 15 minutes. Thereafter, the material was centrifuged and the supernatant was removed. The precipitate was dissolved in 1.6 ml of water and 1.6 ml of isopropanol was added and mixed, followed by allowing to stand at 4°C for 30 minutes. After centrifugation, the supernatant was removed and the precipitate was washed with 75% ethanol. The precipitate was dissolved in 1.6 ml of water. This solution was precipitated with ethanol and the precipitate was washed with 75% ethanol, dried and dissolved in 0.4 ml of water to yield total RNA.

Then, mRNA was prepared using mRNA Isolation Kit (Stratagene). First, 10 ml of Elution Buffer was added to 0.2 ml of total RNA prepared above, and 5 ml of oligo dT solution was further added. After removing the supernatant, the oligo dT was washed three times with High Salt Buffer and twice with Low Salt Buffer and then eluted with Elution Buffer heated to 68°C. This solution was precipitated with ethanol and the precipitate was washed with 75% ethanol, dried and dissolved in 15 µl of water to yield mRNA fraction.

Then, cDNA of PCE I gene was prepared from the mRNA by RT-PCR using Takara RNA PCR Kit (AMV) Ver. 2.1. Thus, oligonucleotide primers having the following sequences were prepared as primers for N- and C-terminals deduced from the genomic PCE I gene sequence determined above and only cDNA of PCE I gene was

amplified by PCR method using 1 µl of mRNA prepared above as a template.

PCEI-CN: 5'-GCGGATCCATGAAGTTCTCCATCATCG-3' (27mer) (SEQ ID NO:112)

PCEI-CC: 5'-GCGGATCCTTACTTGCCTCGCAACCA-3' (27mer) (SEQ ID NO:113)

The RT-PCR reaction was effected under the following conditions. First, the C-terminal primer was added to the reaction mixture and reacted with reverse transcriptase. Then, Taq polymerase (recombinant Taq, Takara Shuzo) and the N-terminal primer were added and the reaction conditions of 94°C for 1 minute, 50°C for 2 minutes and 72°C for 2 minutes were repeated 30 times to amplify. As a result of agarose gel electrophoresis, the amplified fragment was of about 1.0 kbp. The fragment was subcloned into BamHI site of pUC118 and the nucleotide sequence of the fragment was determined according to the method of Example B3 (3). This nucleotide sequence was compared with the genomic nucleotide sequence to determine introns. As a result of this analysis, the entire nucleotide sequence of cDNA of *Phycomyces nitens* PCE I gene was determined.

EXAMPLE G1: Evaluation of fuzz removal action of endoglucanase RCE I expressed in *Humicola insolens* when formulated as detergent

The cellulose containing fabric fuzz removal activity of the endoglucanase RCE I expressed in *Humicola insolens* obtained in Example D4 was evaluated in the following manner. Thus, the cultivation supernatant of the codon optimized endoglucanase RCE I expressed in *Humicola insolens* prepared in Example D4 was used in the fuzz removal treatment of a knitted cotton fabric (6 cm x 8 cm) napped in a large washer containing a surfactant and rubber balls under the conditions as set forth below. The amount of cultivation supernatant required to completely remove the fuzz formed was determined. A cultivation supernatant derived from the untransformed recipient strain was used as a control.

Test machine: Launder Meter L-12 (Daiei Kagaku Seiki MFG., Japan)

Temperature: 40°C

Time: 60 minutes

Reaction volume: 40 ml

Reaction pH: pH 8.5 (10 mM Tris buffer)

(Nonionic surfactant)

Nonipol 100 (Sanyo Kasei Kogyo) 0.15 g/l

(Anionic surfactant)

Shabondama Baby powder soap (Shabondama Soap Japan) 0.55 g/l

The treating liquid contained an appropriate amount of rubber balls together with the endoglucanase solution. The results are shown in Table 7 below.

Table 7

(ml)	Amount of the cultivation supernatant required to remove fuzz of cotton fabric
<i>Humicola insolens</i> MN200-1 (recipient)	Only about 60% of fuzz were removed even by addition of 2 ml.
<i>Humicola insolens</i> pJ14C01 (2-15)	0.1

EXAMPLE G2: Evaluation of waste paper deinking by endoglucanase RCE I expressed in *Humicola insolens*

The centrifuged supernatant of a cultivation broth of codon optimized endoglucanase RCE I expressed in *Humicola insolens* prepared in Example D4 was further subjected to precise filtration (0.45 microns) and the whole amount was lyophilized to yield a crude enzyme powder. This crude enzyme powder had an HEC activity of 1920 units/g. To evaluate the enzymatic deinking power of this crude enzyme, the following enzymatic deinking test was carried out. Newspaper was digested in a shredder and 50 mM phosphate buffer (pH 6.0) was added at 50°C as a concentration of 5% by weight. The newspaper was immersed for 10 minutes to swell. Thereafter, the newspaper was disintegrated by stirring 30,000 times in a JIS standard disintegrator heated at 50°C. To the disintegrated material, the enzyme solution corresponding to 3 mg (100 nkat) and 9 mg (300 nkat) of crude enzyme powder per g of disintegrated material was added. The mixture was thoroughly stirred and incubated at 60°C for 120 minutes.

Thereafter, the enzymatically reacted disintegrated material was stirred 1000 times in a standard disintegrator to yield a homogeneously disintegrated material. One volume of the resulting disintegrated material was diluted with 4 volumes of tap water. A deinking agent (Raisapon 104.1 g/L) and potassium chloride (200 mg/L) were added and subjected to voith flotation cell. Flotation was carried out at 50 deg. for 5 minutes while floated ink was removed out. Thereafter, a hand made sheet was prepared and dried. ISO brightness of the resulting waste paper was measured by a whiteness meter and the area of remaining ink was measured by Quick Scan 35 (Minolta). The analysis results of the three samples, one non-treated zone and two enzymatically treated experimental zones (100 nka/g, 300 nkat/g) by the above procedure are shown in Table 8. From the results, the effectiveness of RCE I on deinking of waste paper was confirmed since the brightness of waste paper obtained from the enzyme experimental zones was superior to the brightness of non-treated waste paper.

Table 8

Concentration of enzyme added	Brightness	Area of remaining ink %
None	46.9	1.19
100 nkat/g	47.6	
300 nkat/g	48.5	1.06

CLAIMS

1. An enzyme having the following properties:
 - a) exhibiting endoglucanase activity; and
 - b) capable of completely removing fuzz from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.
2. The enzyme according to claim 1, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.
3. The enzyme according to claim 1, wherein the enzyme is derived from *Zygomycotina*.
4. The enzyme according to any one of claims 1 to 3, wherein the enzyme is derived from the genus *Rhizopus* and has an average molecular weight of approximately 40 kD as determined by SDS-PAGE.
5. The enzyme according to claim 4, wherein the enzyme has the following properties:
 - the optimum pH for its activity of fuzz removal from regenerated cellulose fabrics: approximately 5; and
 - the optimum temperature for its activity of fuzz removal from regenerated cellulose fabrics: approximately 55°C.
6. The enzyme according to any one of claims 1 to 3, wherein the enzyme is derived from the genus *Mucor* and has an average molecular weight of approximately 41 kD as determined by SDS-PAGE.

7. The enzyme according to claim 6, wherein the enzyme has the following properties:

- the optimum pH for its activity of fuzz removal from regenerated cellulose fabrics: approximately 5-6; and
- the optimum temperature for its activity of fuzz removal from regenerated cellulose fabrics: approximately 50°C.

8. The enzyme according to any one of claims 1 to 3, wherein the enzyme is derived from the genus *Phycomyces* and has an average molecular weight of approximately 45 kD as determined by SDS-PAGE.

9. The enzyme according to claim 8, wherein the enzyme has the following properties:

- the optimum pH for its activity of fuzz removal from regenerated cellulose fabrics: approximately 6; and
- the optimum temperature for its activity of fuzz removal from regenerated cellulose fabrics: approximately 50°C.

10. An enzyme comprising a cellulose binding domain consisting of the following amino acid sequence (I) and exhibiting endoglucanase activity:

Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Gln-Cys-Gly-Gly-Xaa-Xaa-Xaa-Xaa-Gly-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Asn-Xaa-Xaa-Tyr-Xaa-Gln-Cys-Xaa (I) (SEQ ID NO: 18)

wherein Xaa is independently any amino acid residue; Xaa's at positions 20, 21, 22, 23, 24, 30 and 31 may be independently absent; and one of Xaa at position 11 or 33 is Lys and the other is any amino acid residue except Lys.

11. An enzyme comprising a cellulose binding domain consisting of the following

amino acid sequence (II) and exhibiting endoglucanase activity:

Cys-Ser-Xaa-Xaa-Tyr-Xaa-Gln-Cys-Gly-Gly-Xaa-Xaa-Trp-Xaa-Gly-Pro-Thr-Cys-Cys-Xaa
-Xaa-Gly-Xaa-Thr-Cys-Xaa-Xaa-Xaa-Xaa-Asn-Xaa-Xaa-Tyr-Ser-Gln-Cys-Xaa (II)
(SEQ ID NO: 19)

wherein Xaa is independently any amino acid residue; and Xaa's at positions 20, 21, 23, 29 and 30 may be independently absent.

12. The enzyme according to claim 11, wherein one of Xaa at position 11 or 32 is Lys and the other is any amino acid residue except Lys.

13. The enzyme according to claim 10 or 11, wherein the cellulose binding domain consists of the following amino acid sequence (III):

Cys-Ser-X1-X2-Tyr-X3-Gln-Cys-Gly-Gly-X4-X5-Trp-X6-Gly-Pro-Thr-Cys-Cys-X7-X8-Gl
y-X9-Thr-Cys-X10-X11-X12-X13-X14-Asn-X15-X16-Tyr-Ser-Gln-Cys-X17 (III) (SEQ
ID NO: 20)

wherein:

X1 is Lys, Ser or Gln;

X2 is Leu, Ala, Val or Gly;

X3 is Gly, Tyr or Ser;

X4 is Lys or Ile;

X5 is Asn, Asp, Gly or Met;

X6 is Asn, Asp, Ser or Thr;

X7 is Glu, Asp or Thr;

X8 is Ser or Ala;

X9 is Ser or Phe;

X10 is Lys or Val;

X11 is Val, Asp, Ala or Gly;

X12 is Ser, Tyr, Gln or Ala;

X13 is Pro, Glu or Lys, or is absent;

X14 is Asp, Gly or Asn, or is absent;

X15 is Asp, Pro, Lys or Glu;

X16 is Tyr, Phe or Trp;

X17 is Leu, Val or Ile; and

one of X4 or X15 is Lys and the other is any amino acid residue except Lys.

14. The enzyme according to claim 10 or 11, wherein the cellulose binding domain consists of the following amino acid sequence (IV):

Cys-Ser-Lys-X21-Tyr-X22-Gln-Cys-Gly-Gly-Lys-X23-Trp-X24-Gly-Pro-Thr-Cys-Cys-Glu-Ser-Gly-Ser-Thr-Cys-X25-X26-X27-X28-X29-Asn-X30-X31-Tyr-Ser-Gln-Cys-X32

(IV) (SEQ ID NO: 21)

wherein:

X21 is Leu or Ala;

X22 is Gly or Tyr;

X23 is Asn or Asp;

X24 is Asn or Asp;

X25 is Lys or Val;

X26 is Val or Asp;

X27 is Ser or Tyr;

X28 is Pro, or is absent;

X29 is Asp, or is absent;

X30 is Asp or Pro;

X31 is Tyr or Phe; and

X32 is Leu or Val.

15. The enzyme according to claim 14, wherein the cellulose binding domain consists of any one of the amino acid sequences of SEQ ID NOS: 22, 23, and 24.

16. The enzyme according to claim 10 or 11, wherein the cellulose binding domain consists of the following amino acid sequence (V):

Cys-Ser-Ser-Val-Tyr-X41-Gln-Cys-Gly-Gly-Ile-Gly-Trp-X42-Gly-Pro-Thr-Cys-Cys-X43-X

44-Gly-Ser-Thr-Cys-X45-Ala-Gln-X46-X47-Asn-Lys-Tyr-Tyr-Ser-Gln-Cys-X48 (V)
(SEQ ID NO: 25)

wherein:

X41 is Gly or Ser;
X42 is Ser or Thr;
X43 is Glu or Asp;
X44 is Ser or Ala;
X45 is Val or Lys;
X46 is Glu or Lys;
X47 is Gly or Asp; and
X48 is Leu or Ile.

17. The enzyme according to claim 16, wherein the cellulose binding domain consists of the amino acid sequence of SEQ ID NO: 26 or 27.

18. The enzyme according to claim 10 or 11, wherein the cellulose binding domain consists of the amino acid sequence of SEQ ID NO: 28.

19. The enzyme according to claim 10 or 11, wherein the cellulose binding domain is located on its N-terminal side.

20. The enzyme according to any one of claims 10 to 19, wherein the enzyme is capable of removing fuzz completely from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.

21. The enzyme according to any one of claims 10 to 20, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

22. The enzyme according to any one of claims 10 to 21, wherein the enzyme is

derived from *Zygomycotina*.

23. The enzyme according to any one of claims 10 to 22, wherein the enzyme further comprises a part of its linker region consisting of the following amino acid sequence (VI):
Tyr-Xaa-Xaa-Xaa-X51-Gly-Gly-Xaa-X52-Gly (VI) (SEQ ID NO: 31)
wherein Xaa is independently any amino acid residue; and X51 and X52 are independently Ser or Thr.

24. The enzyme according to claim 23, wherein the part of the linker region consists of the following amino acid sequence (VII):
Tyr-X61-Xaa-X62-X51-Gly-Gly-Xaa-X52-Gly (VII) (SEQ ID NO: 32)
wherein:
Xaa is any amino acid residue;
X51 and X52 are independently Ser or Thr;
X61 is Lys or Ser; and
X62 is Ile or Val.

25. The enzyme according to claim 24, wherein Xaa at position 3 is Ala, Ile, Pro or Val, and Xaa at position 8 is Ala, Phe or Lys.

26. The enzyme according to any one of claims 23 to 25, wherein both X51 and X52 are Ser.

27. The enzyme according to claim 23, wherein the part of the linker region consists of any one of the sequences as shown in SEQ ID NOS: 33, 34, 35, 36 and 37.

28. The enzyme according to any one of claims 23 to 27, wherein the part of the linker region is located on the N-terminal side of the catalytic domain.

29. An enzyme which comprises a part of its linker region consisting of the

following amino acid sequence (VI) and exhibits endoglucanase activity:

Tyr-Xaa-Xaa-Xaa-X51-Gly-Gly-Xaa-X52-Gly (VI) (SEQ ID NO: 31)

wherein Xaa is independently any amino acid residue; and X51 and X52 are independently Ser or Thr.

30. The enzyme according to claim 29, wherein the part of the linker region consists of the following amino acid sequence (VII):

Tyr-X61-Xaa-X62-X51-Gly-Gly-Xaa-X52-Gly (VII) (SEQ ID NO: 32)

wherein:

Xaa is any amino acid residue;

X51 and X52 are independently Ser or Thr;

X61 is Lys or Ser; and

X62 is Ile or Val.

31. The enzyme according to claim 30, wherein Xaa at position 3 is Ala, Ile, Pro or Val and Xaa at position 8 is Ala, Phe or Lys.

32. The enzyme according to any one of claims 29 to 31, wherein both X51 and X52 are Ser.

33. The enzyme according to claim 29, wherein the part of the linker region consists of any one of the sequences as shown in SEQ ID NOS: 33, 34, 35, 36 and 37.

34. The enzyme according to any one of claims 29 to 33, wherein the enzyme is capable of removing fuzz completely from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below.

35. The enzyme according to any one of claims 29 to 34, wherein its activity of fuzz removal from regenerated cellulose fabrics at pH 8.5 is 50% or more of its fuzz removal activity at the optimum pH.

36. The enzyme according to any one of claims 29 to 35, wherein the enzyme is derived from *Zygomycotina*.

37. An endoglucanase having the following characteristics:

- i) belonging to family 45;
- ii) being derived from a filamentous fungus; and
- iii) having a cellulose-binding domain located on its N-terminal side.

38. The enzyme according to claim 37, wherein the cellulose-binding domain consists of the amino acid sequence described in any one of claims 10 to 18.

39. The enzyme according to claim 37, wherein the filamentous fungus belongs to the genus *Rhizopus*, the genus *Mucor* or the genus *Phycomyces*.

40. A protein comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11; a modified protein thereof exhibiting endoglucanase activity; or a homologue of said protein or said modified protein.

41. The enzyme according to any one of claims 1 to 39 or the modified protein according to claim 40, wherein the enzyme or the modified protein is modified so that Asn-linked oligosaccharide chains are not added thereto.

42. The modified protein according to claim 41, wherein the modification is the replacement of Asn, Ser and/or Thr with other amino acid(s) and/or the replacement of Xaa with Pro in its Asn-linked glycosylation site(s) Asn-Xaa-Ser/Thr where Xaa is any amino acid residue.

43. The modified protein according to claim 41, wherein the modification is the replacement of Asn with Asp or Gln, and/or the replacement of Ser or Thr with Ala, Gly or

Leu, and/or the replacement of Xaa with Pro in its Asn-linked glycosylation site(s) Asn-Xaa-Ser/Thr where Xaa is any amino acid residue.

44. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1 where the amino acid residue at position 45 or 47 is replaced by other amino acid residue.

45. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1 where the amino acid residue at position 45 or 47 and the amino acid residue(s) at position 90 or 92 and/or position 130 or 132 are replaced by other amino acid residues.

46. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 3 where the amino acid residue at position 45 or 47 is replaced by other amino acid residue.

47. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 3 where the amino acid residue at position 45 or 47 and the amino acid residue(s) at position 92 or 94, position 119 or 121, position 122 or 124 and/or position 158 or 160 are replaced by other amino acid residues.

48. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 5 where the amino acid residue at position 44 or 46 is replaced by other amino acid residue.

49. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 5 where the amino acid residue at position 44 or 46 and the amino acid residue(s) at position 49 or 51, position 121 or 123 and/or position 171 or 173 are replaced by other amino acid residues.

50. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 7 where the amino acid residue at position 50 or 52 is replaced by other amino acid residue.

51. The modified protein according to claim 41, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 9 where the amino acid residue at position 99 or 101 is replaced by other amino acid residue.

52. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 where the cellulose binding domain is modified.

53. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 where a part of the linker domain is modified.

55. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that the cellulose binding domain represents one of the amino acid sequences (I) to (V) described in claims 10, 11, 13, 14 and 16, respectively, and which may have a modification(s) in a region(s) other than said cellulose binding domain.

56. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that a part of the linker region represents the amino acid sequence (VI)

or (VII) described in claim 23 or 24 and which may have a modification(s) in a region(s) other than said part of the linker region.

57. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified so that the cellulose binding domain represents one of the amino acid sequences (I) to (V) described in claims 10, 11, 13, 14 and 16, respectively, and yet modified so that a part of the linker region represents the amino acid sequence (VI) or (VII) described in claim 23 or 24, and which may have a modification(s) in a region(s) other than said cellulose binding domain and said part of the linker region.

58. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified in a region(s) other than the cellulose binding domain and a part of the linker region.

59. The modified protein according to claim 40, wherein said modified protein consists of a modified amino acid sequence represented by SEQ ID NO: 1, 3, 5, 7, 9 or 11 which is modified in a region(s) other than the cellulose binding domain, a part of the linker region and the catalytic domain.

60. A polynucleotide comprising a nucleotide sequence encoding the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59.

61. The polynucleotide according to claim 60, wherein said polynucleotide comprises the DNA sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10 or 12, or a modified sequence thereof.

62. The polynucleotide according to claim 60 or 61, wherein said polynucleotide comprises a nucleotide sequence in which codons have been optimized for a host by

selecting those codons frequently used by the host.

63. The polynucleotide according to claim 62, wherein said nucleotide sequence in which codons have been optimized is the DNA sequence as shown in SEQ ID NO: 13.

64. An expression vector comprising the polynucleotide according to any one of claims 60 to 63.

65. A host cell transformed with the polynucleotide according to any one of claims 60 to 63 or the expression vector according to claim 64.

66. The host cell according to claim 65, wherein said host cell is a yeast or filamentous fungus.

67. The host cell according to claim 66, wherein the yeast belongs to the genus *Saccharomyces*, the genus *Hansenula* or the genus *Pichia*.

68. The host cell according to claim 66, wherein the yeast is *Saccharomyces cerevisiae*.

69. The host cell according to claim 66, wherein the filamentous fungus belongs to the genus *Humicola*, the genus *Aspergillus*, the genus *Trichoderma*, the genus *Acremonium* or the genus *Fusarium*.

70. The host cell according to claim 66, wherein the filamentous fungus is *Humicola insolens*, *Aspergillus niger* or *Trichoderma viride*.

71. A method for producing the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59, comprising cultivating the host cell according to any one of claims 65 to 70 and recovering the enzyme, protein, modified protein or homologue

from said host cell and/or the resultant cultivation broth.

72. An endoglucanase produced by the method according to claim 71.

73. A cellulase preparation comprising the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72.

74. A method of treating cellulose-containing fabrics, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

75. A method of reducing the rate at which cellulose-containing fabrics become fuzzy or for reducing fuzzing in cellulose-containing fabrics, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

76. A method of weight loss treatment for cellulose-containing fabrics to improve its touch and appearance, comprising a step of contacting the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

77. A method of providing color clarification of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

78. A method of providing a localized variation in color of colored cellulose-containing fabrics, comprising a step of treating the colored cellulose-containing

fabrics with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

79. A method of reducing the rate at which cellulose-containing fabrics become stiff or reducing stiffness in cellulose-containing fabrics, comprising a step of treating the cellulose-containing fabrics with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

80. The method according to any one of the claims 74 to 79, wherein the treatment of the fabrics is performed through soaking, washing or rinsing the fabrics.

81. An additive to detergent comprising the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73 in a non-scattering granular form or a stabilized liquid form.

82. A detergent composition comprising the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

83. A method of improving the freeness of a paper pulp, comprising a step of treating the paper pulp with the enzyme, protein, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73.

84. A method of deinking a waste paper, comprising a step of treating the waste paper with the endoglucanase, modified protein or homologue according to any one of claims 1 to 59 and 72 or the cellulase preparation according to claim 73 in the presence of a deinking agent.

85. A method of improving the digestibility of an animal feed, comprising a step of

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

ABSTRACT

It is an object of the present invention to provide enzymes that have high endoglucanase activity and yet exhibit high activity even under alkaline conditions, and genes encoding the same. The enzyme according to the invention has the following properties: a) exhibiting endoglucanase activity; and b) capable of completely removing fuzz from regenerated cellulose fabrics at a concentration of 1 mg of the protein/L or below. The enzyme of the invention having endoglucanase activity is a protein comprising the amino acid sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9 or 11; a modified protein thereof exhibiting endoglucanase activity; or a homologue of the protein or the modified protein.

09/80

1 / 3

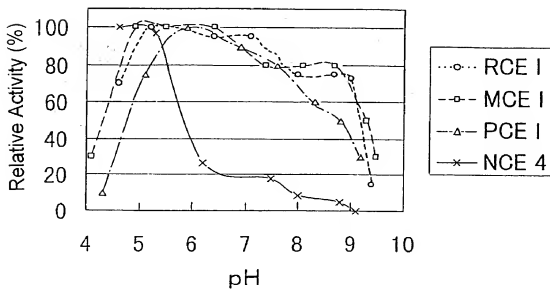


FIG. 1

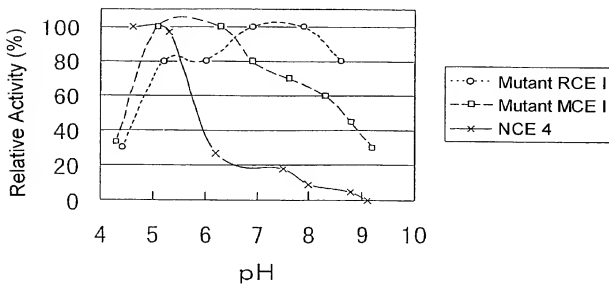


FIG. 2

2/3

Codon	Count	Codon	Count	Codon	Count	Codon	Count
TTT-Phe	2	TCT-Ser	24	TAT-Tyr	4	TGT-Cys	20
TTC-Phe	6	TCC-Ser	9	TAC-Tyr	8	TGC-Cys	6
TTA-Leu	0	TCA-Ser	2	TAA-***	1	TGA-***	0
TTG-Leu	3	TCG-Ser	1	TAG-***	0	TGG-Trp	10
CTT-Leu	8	CCT-Pro	7	CAT-His	1	CCT-Arg	1
CTC-Leu	3	CCC-Pro	5	CAC-His	1	CGC-Arg	1
CTA-Leu	0	CCA-Pro	1	CAA-Gln	9	CGA-Arg	0
CTG-Leu	1	CCG-Pro	0	CAG-Gln	1	CGG-Arg	0
ATT-Ile	6	ACT-Thr	19	AAT-Asn	10	AGT-Ser	6
ATC-Ile	3	ACC-Thr	7	AAC-Asn	16	AGC-Ser	11
ATA-Ile	0	ACA-Thr	2	AAA-Lys	10	AGA-Arg	3
ATG-Met	6	ACG-Thr	1	AAG-Lys	17	AGG-Arg	0
GTT-Val	4	GCT-Ala	17	GAT-Asp	7	GGT-Gly	34
GTC-Val	7	GCC-Ala	12	GAC-Asp	7	GGC-Gly	8
GTA-Val	3	GCA-Ala	2	GAA-Glu	12	GGA-Gly	2
GTG-Val	0	GCG-Ala	0	GAG-Glu	0	GGG-Gly	0

FIG. 3

Codon	Count	Codon	Count	Codon	Count	Codon	Count
TTT-Phe	0	TCT-Ser	2	TAT-Tyr	4	TGT-Cys	0
TTC-Phe	19	TCC-Ser	9	TAC-Tyr	18	TGC-Cys	18
TTA-Leu	0	TCA-Ser	0	TAA-***	1	TGA-***	0
TTG-Leu	0	TCG-Ser	7	TAG-***	0	TGG-Trp	10
CTT-Leu	1	CCT-Pro	3	CAT-His	0	CCT-Arg	4
CTC-Leu	13	CCC-Pro	13	CAC-His	7	CGC-Arg	13
CTA-Leu	0	CCA-Pro	0	CAA-Gln	1	CGA-Arg	0
CTG-Leu	8	CCG-Pro	8	CAG-Gln	17	CGG-Arg	0
ATT-Ile	3	ACT-Thr	0	AAT-Asn	1	AGT-Ser	0
ATC-Ile	13	ACC-Thr	25	AAC-Asn	33	AGC-Ser	12
ATA-Ile	0	ACA-Thr	0	AAA-Lys	0	AGA-Arg	0
ATG-Met	12	ACG-Thr	2	AAG-Lys	17	AGG-Arg	4
GTT-Val	3	GCT-Ala	10	GAT-Asp	8	GGT-Gly	12
GTC-Val	19	GCC-Ala	29	GAC-Asp	19	GGC-Gly	30
GTA-Val	0	GCA-Ala	0	GAA-Glu	0	GGA-Gly	0
GTG-Val	2	GCG-Ala	2	GAG-Glu	20	GGG-Gly	0

FIG. 4

3/3

Codon	Count	Codon	Count	Codon	Count	Codon	Count
TTT-Phe	2	TCT-Ser	3	TAT-Tyr	2	TGT-Cys	1
TTC-Phe	14	TCC-Ser	2	TAC-Tyr	18	TGC-Cys	10
TTA-Leu	1	TCA-Ser	0	TAA-***	0	TGA-***	1
TTG-Leu	3	TCG-Ser	14	TAG-***	0	TGG-Trp	12
CTT-Leu	4	CCT-Pro	6	CAT-His	0	CGT-Arg	1
CTC-Leu	16	CCC-Pro	15	CAC-His	7	CGC-Arg	16
CTA-Leu	0	CCA-Pro	0	CAA-Gln	2	CGA-Arg	0
CTG-Leu	3	CCG-Pro	11	CAG-Gln	19	CGG-Arg	2
ATT-Ile	5	ACT-Thr	7	AAT-Asn	4	AGT-Ser	0
ATC-Ile	16	ACC-Thr	30	AAC-Asn	25	AGC-Ser	11
ATA-Ile	0	ACA-Thr	0	AAA-Lys	0	AGA-Arg	0
ATG-Met	6	ACG-Thr	6	AAG-Lys	12	AGG-Arg	2
GTT-Val	4	GCT-Ala	13	GAT-Asp	2	GGT-Gly	12
GTC-Val	20	GCC-Ala	45	GAC-Asp	17	GGC-Gly	24
GTA-Val	0	GCA-Ala	0	GAA-Glu	1	GGA-Gly	1
GTG-Val	2	GCG-Ala	7	GAG-Glu	20	GGG-Gly	0

FIG. 5

Codon	Count	Codon	Count	Codon	Count	Codon	Count
TTT-Phe	1	TCT-Ser	2	TAT-Tyr	0	TGT-Cys	0
TTC-Phe	15	TCC-Ser	12	TAC-Tyr	6	TGC-Cys	20
TTA-Leu	0	TCA-Ser	0	TAA-***	0	TGA-***	0
TTG-Leu	1	TCG-Ser	4	TAG-***	1	TGG-Trp	9
CTT-Leu	2	CCT-Pro	7	CAT-His	1	CGT-Arg	3
CTC-Leu	7	CCC-Pro	9	CAC-His	1	CGC-Arg	7
CTA-Leu	0	CCA-Pro	2	CAA-Gln	1	CGA-Arg	0
CTG-Leu	3	CCG-Pro	6	CAG-Gln	12	CGG-Arg	1
ATT-Ile	2	ACT-Thr	5	AAT-Asn	3	AGT-Ser	1
ATC-Ile	4	ACC-Thr	17	AAC-Asn	11	AGC-Ser	13
ATA-Ile	0	ACA-Thr	1	AAA-Lys	0	AGA-Arg	0
ATG-Met	2	ACG-Thr	2	AAG-Lys	10	AGG-Arg	1
GTT-Val	2	GCT-Ala	9	GAT-Asp	4	GGT-Gly	5
GTC-Val	11	GCC-Ala	17	GAC-Asp	13	GGC-Gly	26
GTA-Val	0	GCA-Ala	0	GAA-Glu	0	GGA-Gly	2
GTG-Val	4	GCG-Ala	2	GAG-Glu	6	GGG-Gly	0

FIG. 6

Attorney's Docket No.: _____

DECLARATION, POWER OF ATTORNEY AND PETITION

I (We), the undersigned inventor(s), hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I (We) believe that I am (we are) the original, first, and joint (sole) inventor(s) of the subject matter which is claimed and for which a patent is sought on the invention entitled

ENDOGLUCANASES AND CELLULASE PREPARATIONS CONTAINING THE
SAME

the specification of which

☐ is attached hereto.

☐ was filed on _____ as

Application Serial No. _____

and amended on _____.

☒ was filed as PCT international application

Number PCT/JP99/05884

on October 25, 1999

and was amended under PCT Article 19

on _____ (if applicable).

I (We) hereby state that I (We) have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above; that I (We) do not know and do not believe that this invention was ever known or used before my invention or discovery thereof, or patented or described in any printed publication in any country before my invention or discovery thereof, or more than one year prior to this application, or in public use or on sale in the United States for more than one year prior to this application; that this invention or discovery has not been patented or made the subject of an inventor's certificate in any country foreign to the United States on an application filed by me or my legal representatives or assigns more than twelve months before this application.

I (We) acknowledge the duty to disclose information known to be material to

09/807933

JCO8 Rec'd PCT/PTO 20 APR 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the patent application of:

Yuko NAKAMURA et al.

Serial No: NEW - Based on PCT/JP99/05884

Filed: April 20, 2001

Title: ENDOGLUCANASES AND CELLULASE PREPARATIONS CONTAINING THE
SAME

Group Art Unit:

Examiner:

RE: CHANGE OF CORRESPONDENCE AND FEE ADDRESSESHonorable Commissioner of Patents
and Trademarks

Washington, D.C. 20231

April 20, 2001

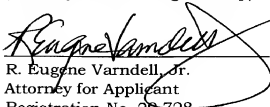
Dear Sir:

Effective April 28, 2001, please change both the correspondence and fee
addresses in this application to the following address:

VARNDELL & VARNDELL, PLLC
106-A South Columbus Street
Alexandria, VA 22314

Our telephone and facsimile numbers remain the same.

Respectfully submitted,
VARNDELL & VARNDELL, PLLC
(formerly Varndell Legal Group)


R. Eugene Varndell, Jr.
Attorney for Applicant
Registration No. 29,728

Atty. Docket No.: VX012273 PCT
106-A S. Columbus St.
Alexandria, VA 22314
(703) 683-9730

Application Serial No.	Filing Date	Status (pending, patented, abandoned)

_____	_____	_____
_____	_____	_____

And I (We) hereby appoint:

R. Eugene Varndell, Jr., Registration No. 29,728; and Debra Shoemaker, Registration No. 47,941

I(We) hereby request that all correspondence regarding this application be sent to the firm of Varndell & Varndell, PLLP whose Post office address is: Suite 220, 1150 South Washington Street, Alexandria, VA 22314 U.S.A.

I (We) declare further that all statements made herein of my (our) knowledge are true and that all statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

100 Yuko NAKAMURA
NAME OF FIRST SOLE INVENTOR

Yuko Nakamura
Signature of Inventor

April 13, 2001
Date

Residence: Saitama, Japan JPX

Citizen of: Japan
Post Office Address: c/o Bioscience
Labs., Meiji Seika Kaisha, Ltd.,
5-3-1, Chiyoda, Sakado-shi,
Saitama 350-0289 Japan

200

Tatsuki MORIYA

NAME OF SECOND JOINT INVENTOR

Tatsuki Moriya

Signature of Inventor

April 16, 2001

Date

Residence: Kanagawa, Japan *TPX*Citizen of: Japan

Post Office Address: _____

c/o Pharmaceutical TechnologyLabs., Meiji Seika Kaisha, Ltd.,788, Kayama, Odawara-shi,Kanagawa 250-0852 Japan

300

Yuko BABA

NAME OF THIRD JOINT INVENTOR

Yuko Baba

Signature of Inventor

April 13, 2001

Date

Residence: Saitama, Japan *TPX*Citizen of: JapanPost Office Address: c/o BioscienceLabs., Meiji Seika Kaisha, Ltd.,5-3-1, Chiyoda, Sakado-shi,Saitama 350-0289 Japan

400

Koji YANAI

NAME OF FOURTH JOINT INVENTOR

Koji Yanai

Signature of Inventor

April 16, 2001

Date

Residence: Kanagawa, Japan *TPX*Citizen of: Japan

Post Office Address: _____

c/o Pharmaceutical TechnologyLabs., Meiji Seika Kaisha, Ltd.,788, Kayama, Odawara-shi,Kanagawa 250-0852 Japan

500 Naomi SUMIDA
NAME OF FIFTH JOINT INVENTOR

Naomi Sumida
Signature of Inventor

April 16, 2001
Date

Residence: Kanagawa, Japan *TPX*

Citizen of: Japan

Post Office Address: _____
c/o Pharmaceutical Technology
Labs., Meiji Seika Kaisha, Ltd.,
788, Kayama, Odawara-shi,
Kanagawa 250-0852 Japan

600 Tomoko NISHIMURA
NAME OF SIXTH JOINT INVENTOR

Tomoko Nishimura
Signature of Inventor

April 13, 2001
Date

Residence: Saitama, Japan *TPX*

Citizen of: Japan

Post Office Address: c/o Bioscience
Labs., Meiji Seika Kaisha, Ltd.,
5-3-1, Chiyoda, Sakado-shi,
Saitama 350-0289 Japan

700 Kouichirou MURASHIMA
NAME OF SEVENTH JOINT INVENTOR

Koichiro Murashima
Signature of Inventor

April 13, 2001
Date

Residence: Saitama, Japan *TPX*

Citizen of: Japan

Post Office Address: c/o Bioscience
Labs., Meiji Seika Kaisha, Ltd.,
5-3-1, Chiyoda, Sakado-shi,
Saitama 350-0289 Japan

800 Akitaka NAKANE
NAME OF EIGHTH JOINT INVENTOR

Akitaka Nakane
Signature of Inventor

April 13, 2001
Date

Residence: Saitama, Japan *TPX*

Citizen of: Japan

Post Office Address: c/o Bioscience
Labs., Meiji Seika Kaisha, Ltd.,
5-3-1, Chiyoda, Sakado-shi,
Saitama 350-0289 Japan

900 Takashi YAGUCHI
NAME OF NINETH JOINT INVENTOR

Takashi Yaguchi
Signature of Inventor

April 17, 2001
Date

Residence: Kanagawa, Japan *TPX*

Citizen of: Japan

Post Office Address: c/o Pharmaceutical Research Center,
Meiji Seika Kaisha, Ltd., 760,
Morooka-cho, Kouhoku-ku,
Yokohama-shi, Kanagawa 222-8567
Japan

1000 Junichiro KOGA
NAME OF TENTH JOINT INVENTOR

Junichiro Koga
Signature of Inventor

April 13, 2001
Date

Residence: Saitama, Japan *TPX*

Citizen of: Japan

Post Office Address: c/o Bioscience
Labs., Meiji Seika Kaisha, Ltd.,
5-3-1, Chiyoda, Sakado-shi,
Saitama 350-0289 Japan

1180 Takeshi MURAKAMI

NAME OF ELEVENTH JOINT INVENTOR

Takeshi Murakami

Signature of Inventor

April 16, 2001

Date

Residence: Kanagawa, Japan *TPX*

Citizen of: Japan

Post Office Address: _____

c/o Pharmaceutical Technology

Labs., Meiji Seika Kaisha, Ltd.,

788, Kayama, Odawara-shi,

Kanagawa 250-0852 Japan

1280 Toshiaki KONO

NAME OF TWELFTH JOINT INVENTOR

Toshiaki Kono

Signature of Inventor

April 13, 2001

Date

Residence: Saitama, Japan *TPX*

Citizen of: Japan

Post Office Address: c/o Bioscience

Labs., Meiji Seika Kaisha, Ltd.,

5-3-1, Chiyoda, Sakado-shi,

Saitama 350-0289 Japan

SEQUENCE LISTING

<110> MEIJI SEIKA KAISHA, LTD.

<120> Endoglucanase and cellulase composition containing the
same

<130> 121659PX

<140>

<141>

<150> JP302387/1998

<151> 1998-10-23

<160> 113

<170> PatentIn Ver. 2.0

<210> 1

<211> 328

<212> PRT

<213> Rhizopus oryzae CP96001

<220>

<221> sig_peptide

<222> (-23)... (-1)

<221> mat_peptide

<222> (1)... (315)

<400> 1

Met Lys Phe Ile Thr Ile Ala Ser Ser Ala Leu Leu Ala Leu Ala Leu
 -20 -15 -10
 Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys Leu Tyr Gly Gln
 -5 1 5
 Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
 10 15 20 25
 Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly
 30 35 40
 Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr
 45 50 55
 Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr
 60 65 70
 Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser
 75 80 85
 Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly
 90 95 100 105
 Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala
 110 115 120
 Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser
 125 130 135
 Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser
 140 145 150
 Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp
 155 160 165
 Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser
 170 175 180 185
 Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe

3/73

	190		195		200
Thr	Ser	Thr	Ser	Val	Ala
		Gly	Lys	Lys	Met
			Val	Val	Gln
			Val	Val	Thr
					Asn
	205		210		215
Thr	Gly	Gly	Asp	Leu	Gly
		Ser	Ser	Thr	Gly
			Ala	His	Phe
			Asp	Leu	Gln
	220		225		230
Met	Pro	Gly	Gly	Gly	Val
		Gly	Ile	Phe	Asn
			Gly	Cys	Ser
			Ser	Ser	Gln
					Trp
	235		240		245
Gly	Ala	Pro	Asn	Asp	Gly
		Trp	Gly	Ser	Arg
			Tyr	Gly	Gly
			Ile	Ser	Ser
	250		255		260
					265
Ala	Ser	Asp	Cys	Ser	Ser
		Leu	Pro	Ser	Ala
			Leu	Gln	Ala
			Gly	Cys	Lys
		270		275	280
Trp	Arg	Phe	Asn	Trp	Phe
		Lys	Asn	Ala	Asp
			Asn	Pro	Ser
			Met	Thr	Tyr
	285		290		295
Lys	Glu	Val	Thr	Cys	Pro
		Lys	Glu	Ile	Thr
		Ala	Lys	Thr	Gly
			Cys	Ser	
	300		305		310
Arg	Lys				
	315				

<210> 2

<211> 1017

<212> DNA

<213> Rhizopus oryzae CP96001

<220>

<221> sig_peptide

<222> (1)... (69)

<221> mat_peptide

<222> (70)... (1017)

<400> 2

atg aag ttt att act att gcc tct tcc gct ctc ttg gct ctc gcc ctc	48
Met Lys Phe Ile Thr Ile Ala Ser Ser Ala Leu Leu Ala Leu Ala Leu	
-20 -15 -10	
ggc act gaa atg gcc tct gct gct gaa tgt agc aaa ttg tat ggt caa	96
Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys Leu Tyr Gly Gln	
-5 1 5	
tgt ggt ggt aag aac tgg aat ggc cct act tgt tgt gaa tct gga tcc	144
Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser	
10 15 20 25	
acc tgt aaa gla agc aac gat tac tac tct caa tgt ctt ccc tct gga	192
Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly	
30 35 40	
agc agt ggc aat aaa tct tct gaa agt gct cac aag aag act acc act	240
Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr	
45 50 55	
gct gct cac aag aag act act acc gct gct cat aaa aag act acc act	288
Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr	
60 65 70	
gct cct gct aag aag act aca act gtt gcc aaa gct tcc acc cct tct	336
Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser	
75 80 85	
aac tct agc tct agc tcc agc ggc aaa tat tcc gct gtc tct ggt ggt	384
Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly	
90 95 100 105	
gcc tct ggt aac ggt gtc act act cgt tat tgg gat tgc tgt aag gcc	432
Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala	
110 115 120	
tcc tgt agc tgg ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc	480
Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser	

125	130	135	
lgt aac aaa gat ggt gtc act gcc ctt agt gac agc aat gcc caa agt			528
Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser			
140	145	150	
ggc lgt aac ggt ggt aac agt tac atg lgt aac gac aac caa cct tgg			576
Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp			
155	160	165	
gct gta aac gac aac ctt gcc tat ggt ttc gct gct gct gcc atc agt			624
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser			
170	175	180	185
ggt ggt ggt gaa tct cgc tgg tgc lgt tct lgt ttc gaa ctt act ttc			672
Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe			
190	195	200	
act tct acc tct gtt gct ggt aag aag atg gtt gtc caa gtc act aac			720
Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn			
205	210	215	
act ggt ggt gat ctt ggc tcc tct act ggt gct cac ttt gac ttg caa			768
Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln			
220	225	230	
atg ccc ggt ggt ggt gtt ggt att ttc aat ggt lgt tcc agc caa tgg			816
Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp			
235	240	245	
ggt gct ccc aat gac ggt tgg ggc tca aga tac ggt ggt att tct tct			864
Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser			
250	255	260	265
gca tct gac tgc tct agt ctt cct tcc gca ctc caa gct ggt lgt aaa			912
Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys			
270	275	280	
tgg aga ttc aac tgg ttc aag aac gct gat aac cca agc atg act tac			960

6/73

Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr
 285 290 295
 aag gaa gtt acc tgt cct aag gaa atc acc gcc aag aca ggt tgt tca 1008
 Lys Glu Val Thr Cys Pro Lys Glu Ile Thr Ala Lys Thr Gly Cys Ser
 300 305 310
 aga aaa taa 1017
 Arg Lys
 315

<210> 3

<211> 366

<212> PRT

<213> Rhizopus oryzae CP96001

<220>

<221> sig_peptide

<222> (-23)... (-1)

<221> mat_peptide

<222> (1)... (343)

<400> 3

Met Lys Phe Ile Thr Ile Thr Ser Ser Ala Leu Leu Ala Leu Ala Leu
 -20 -15 -10
 Gly Thr Glu Met Ala Ser Ala Ala Lys Cys Ser Lys Leu Tyr Gly Gln
 -5 1 5
 Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
 10 15 20 25
 Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu
 30 35 40

Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys
 45 50 55
 Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
 60 65 70
 Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser
 75 80 85
 Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr
 90 95 100 105
 Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser
 110 115 120
 Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn
 125 130 135
 Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp
 140 145 150
 Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp
 155 160 165
 Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly
 170 175 180 185
 Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp
 190 195 200
 Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu
 205 210 215
 Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser
 220 225 230
 Val Ala Gly Lys Lys Met Val Ile Gln Val Thr Asn Thr Gly Gly Asp
 235 240 245
 Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
 250 255 260 265
 Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn

8/73

	270		275		280
Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys					
	285		290		295
Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn					
	300		305		310
Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys Glu Val Thr					
	315		320		325
Cys Pro Lys Glu Ile Thr Ala Lys Thr Gly Cys Ser Arg Lys					
330		335		340	

<210> 4

<211> 1101

<212> DNA

<213> Rhizopus oryzae CP96001

<220>

<221> sig_peptide

<222> (1)... (69)

<221> mat_peptide

<222> (70)... (1101)

<400> 4

atg aag ttt att act att acc tct tcc gct ctc ttg gct ctc gcc ctt	48
Met Lys Phe Ile Thr Ile Thr Ser Ser Ala Leu Leu Ala Leu Ala Leu	
-20	-15
ggg act gaa atg gcc tct gct gct aaa tgt agc aag ctc tat ggt caa	96
Gly Thr Glu Met Ala Ser Ala Ala Lys Cys Ser Lys Leu Tyr Gly Gln	
-5	1
tgt ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc	144
Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser	

9/73

10	15	20	25	
acc tgt aaa gla agc aac gat tac tac tct caa tgt ctt gcc cct gaa	192			
Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu				
30	35	40		
agc aac ggc aat aag tct tct gaa tgt agc aag ttg tat ggt caa tgt	240			
Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys				
45	50	55		
ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc acc	288			
Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr				
60	65	70		
tgt aaa gla agc aac gat tac tac tct caa tgt ctt gcc cct gaa agc	336			
Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser				
75	80	85		
aat ggc aat aaa act tct gaa agc gct cat aaa acg act act acc act	384			
Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr				
90	95	100	105	
gct ccc gct aag gaa att aca act act gcc aaa gct tca aac tct tct	432			
Ala Pro Ala Lys Glu Ile Thr Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser				
110	115	120		
aac tct agc ggc aaa tac tcc att gtc tct ggt ggt gcc tct ggt aac	480			
Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn				
125	130	135		
ggt gtc act act cgt tat tgg gat tgc tgt aag gcc tcc tgt agc tgg	528			
Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp				
140	145	150		
ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc tgt aac aaa gat	576			
Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp				
155	160	165		
ggt gtc act gcc cit agt gac agc aat gtc caa agt ggc tgt aac ggt	624			

Gly	Val	Thr	Ala	Leu	Ser	Asp	Ser	Asn	Val	Gln	Ser	Gly	Cys	Asn	Gly	
170						175				180					185	
ggg	aac	agc	tac	atg	tgt	aac	gac	aac	cag	cct	tgg	gct	gta	aac	gat	672
Gly	Asn	Ser	Tyr	Met	Cys	Asn	Asp	Asn	Gln	Pro	Trp	Ala	Val	Asn	Asp	
				190					195					200		
aat	ctt	gcc	tat	ggc	ttc	gct	gct	gct	gcc	atc	agt	ggc	ggc	ggc	gaa	720
Asn	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Ala	Ala	Ile	Ser	Gly	Gly	Gly	Glu	
				205				210					215			
tct	cgc	tgg	tgc	tgt	tct	tgt	ttc	gaa	ctt	act	ttc	act	tct	acc	tct	768
Ser	Arg	Trp	Cys	Cys	Ser	Cys	Phe	Glu	Leu	Thr	Phe	Thr	Ser	Thr	Ser	
				220			225					230				
ggt	gct	ggc	aag	aag	atg	gtt	atc	caa	gtc	act	aac	act	ggc	ggc	gat	816
Val	Ala	Gly	Lys	Lys	Met	Val	Ile	Gln	Val	Thr	Asn	Thr	Gly	Gly	Asp	
		235				240				245						
ctt	ggc	tcc	tct	act	ggc	gct	cac	ttt	gac	tgc	caa	atg	ccc	ggc	ggc	864
Leu	Gly	Ser	Ser	Thr	Gly	Ala	His	Phe	Asp	Leu	Gln	Met	Pro	Gly	Gly	
250					255					260					265	
ggc	gtt	ggc	att	ttc	aat	ggc	tgc	tcc	aag	caa	tgg	ggc	gct	ccc	aat	912
Gly	Val	Gly	Ile	Phe	Asn	Gly	Cys	Ser	Lys	Gln	Trp	Gly	Ala	Pro	Asn	
				270					275					280		
gac	ggc	tgg	ggc	tgc	aga	tac	ggc	ggc	att	tct	tct	gca	tct	gac	tgc	960
Asp	Gly	Trp	Gly	Ser	Arg	Tyr	Gly	Gly	Ile	Ser	Ser	Ala	Ser	Asp	Cys	
				285					290					295		
tct	agt	ctt	cct	tcc	gca	cic	caa	gct	ggc	tgt	aaa	tgg	aga	ttc	aac	1008
Ser	Ser	Leu	Pro	Ser	Ala	Leu	Gln	Ala	Gly	Cys	Lys	Trp	Arg	Phe	Asn	
		300					305					310				
tgg	ttc	aag	aac	gct	gat	aac	cca	agc	atg	act	tac	aag	gaa	gtt	acc	1056
Trp	Phe	Lys	Asn	Ala	Asp	Asn	Pro	Ser	Met	Thr	Tyr	Lys	Glu	Val	Thr	
		315				320					325					

tgt ccc aag gaa atc acc gcc aag aca ggt tgt tca aga aaa taa 1101

Cys Pro Lys Glu Ile Thr Ala Lys Thr Gly Cys Ser Arg Lys

330

335

340

<210> 5

<211> 360

<212> PRT

<213> Rhizopus oryzae CP96001

<220>

<221> sig_peptide

<222> (-23)... (-1)

<221> mat_peptide

<222> (1)... (337)

<400> 5

Met Lys Phe Leu Thr Ile Ala Ser Ser Ala Ile Leu Ala Leu Ala Val

-20

-15

-10

Gly Thr Glu Met Ala His Ala Ala Glu Cys Ser Lys Ala Tyr Tyr Gln

-5

1

5

Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser

10

15

20

25

Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro

30

35

40

Asn Glu Asn Leu Thr Ser Thr Asn Lys Ser Ser His Lys Thr Thr Thr

45

50

55

Thr Glu Ser Ala Lys Lys Thr Thr Thr Lys Gly Ser Lys Lys Thr

60

65

70

Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Glu Ala Ser Lys

12/73

75					80					85					
Lys	Thr	Thr	Thr	Thr	Glu	Ala	Ser	Lys	Lys	Thr	Thr	Thr	Thr	Lys	
90					95					100				105	
Lys	Ala	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Thr	Asn
					110					115				120	
Tyr	Ser	Ala	Val	Ser	Gly	Gly	Ala	Ser	Gly	Asn	Gly	Glu	Thr	Thr	Arg
					125					130				135	
Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Ser	Trp	Pro	Gly	Lys	Ala	Asp
					140					145				150	
Val	Thr	Ser	Pro	Val	Gly	Ser	Cys	Asn	Lys	Asp	Gly	Lys	Thr	Leu	Ala
					155					160				165	
Asp	Asn	Asn	Thr	Gln	Asn	Gly	Cys	Val	Gly	Gly	Ser	Ser	Tyr	Thr	Cys
170					175					180				185	
Asn	Asp	Asn	Gln	Pro	Trp	Val	Val	Ser	Asp	Asp	Leu	Ala	Tyr	Gly	Phe
					190					195				200	
Ala	Ala	Ala	Ser	Ile	Ser	Gly	Gly	Ser	Glu	Ala	Thr	Trp	Cys	Cys	Ala
					205					210				215	
Cys	Phe	Glu	Leu	Thr	Phe	Thr	Ser	Thr	Ala	Val	Lys	Gly	Lys	Lys	Met
					220					225				230	
Val	Val	Gln	Val	Thr	Asn	Thr	Gly	Ser	Asp	Leu	Gly	Ser	Asn	Thr	Gly
					235					240				245	
Ala	His	Phe	Asp	Leu	Gln	Met	Pro	Gly	Gly	Gly	Val	Gly	Ile	Tyr	Asn
250					255					260				265	
Gly	Cys	Ala	Thr	Gln	Trp	Gly	Ala	Pro	Thr	Asp	Gly	Trp	Gly	Ala	Arg
					270					275				280	
Tyr	Gly	Gly	Val	Ser	Ser	Ala	Ser	Asp	Cys	Ser	Asn	Leu	Pro	Ser	Ala
					285					290				295	
Leu	Gln	Ala	Gly	Cys	Lys	Trp	Arg	Phe	Gly	Trp	Phe	Lys	Asn	Ala	Asp
					300					305				310	

Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr

315

320

325

Ala Lys Ser Gly Cys Ser Arg Lys

330

335

<210> 6

<211> 1083

<212> DNA

<213> *Rhizopus oryzae* CP96001

<220>

<221> sig_peptide

<222> (1)... (69)

<221> mat_peptide

<222> (70)... (1083)

<400> 6

atg aag ttc ctt acc att gcc tcc tcc gct atc tlg gca ctt gcc gtc 48

Met Lys Phe Leu Thr Ile Ala Ser Ser Ala Ile Leu Ala Leu Ala Val

-20

-15

-10

ggc act gaa atg gcc cat gct gct gaa tgt agc aag gct tac tac caa 96

Gly Thr Glu Met Ala His Ala Ala Glu Cys Ser Lys Ala Tyr Tyr Gln

-5

1

5

tgt ggt ggt aag aac tgg gat gga cct acc tgc tgt gaa tct ggc tct 144

Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser

10

15

20

25

act tgc gtt gat tat cct gac aat cct ttc tac tcc caa tgt gtt ccc 192

Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro

30

35

40

aat gaa aac ctc acc tcc act aac aaa tct tct cac aaa acc acc act 240



gcc gct gct tcc att tct ggt ggt agc gaa gct act tgg tgt tgt gcc 720
 Ala Ala Ala Ser Ile Ser Gly Gly Ser Glu Ala Thr Trp Cys Cys Ala
 205 210 215
 tgt ttc gaa ctc aca ttc acc tct act gcc gtc aag ggt aag aag atg 768
 Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met
 220 225 230
 gtt gtt caa gta acc aac act ggt tct gac ctt ggc tct aac act ggt 816
 Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly
 235 240 245
 gct cac ttt gac ttg caa atg ccc ggt ggt ggt gtt ggt atc tac aat 864
 Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn
 250 255 260 265
 ggt tgt gcc act caa tgg ggt gct ccc acc gat ggt tgg ggt gca aga 912
 Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg
 270 275 280
 tac ggc ggt gtt tct tct gcc tct gac tgt tct aac ctt cct tct gcc 960
 Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala
 285 290 295
 ctt caa gct ggt tgt aag tgg aga ttc ggc tgg ttc aaa aac gct gat 1008
 Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp
 300 305 310
 aac cca acc atg acc tac aaa caa gtt acc tgt ccc aag gct atc act 1056
 Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr
 315 320 325
 gcc aag tct ggc tgt tca aga aaa taa 1083
 Ala Lys Ser Gly Cys Ser Arg Lys
 330 335

<211> 338

<212> PRT

<213> *Mucor circinelloides* CP99001

<220>

<221> sig_peptide

<222> (-22)... (-1)

<221> mat_peptide

<222> (1)... (316)

<400> 7

Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu

-20

-15

-10

Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys

-5

1

5

10

Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr

15

20

25

Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly

30

35

40

Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser

45

50

55

Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr

60

65

70

Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr

75

80

85

90

Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ala Gly Tyr Lys Val

95

100

105

Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp

110

115

120

Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly

125					130					135					
Pro	Val	Asp	Thr	Cys	Ala	Ser	Asn	Gly	Ile	Ser	Leu	Leu	Asp	Ala	Asn
140					145					150					
Ala	Gln	Ser	Gly	Cys	Asn	Gly	Gly	Asn	Gly	Phe	Met	Cys	Asn	Asn	Asn
155					160					165					170
Gln	Pro	Trp	Ala	Val	Asn	Asp	Glu	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Ala
175					180					185					
Ser	Ile	Ala	Gly	Ser	Asn	Glu	Ala	Gly	Trp	Cys	Cys	Gly	Cys	Tyr	Glu
190					195					200					
Leu	Thr	Phe	Thr	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Lys	Met	Val	Val	Gln
205					210					215					
Val	Thr	Asn	Thr	Gly	Gly	Asp	Leu	Gly	Ser	Asn	His	Phe	Asp	Leu	Gln
220					225					230					
Met	Pro	Gly	Gly	Gly	Val	Gly	Ile	Phe	Asn	Gly	Cys	Ala	Ala	Gln	Trp
235					240					245					250
Gly	Ala	Pro	Asn	Asp	Gly	Trp	Gly	Ala	Arg	Tyr	Gly	Gly	Val	Ser	Ser
255					260					265					
Val	Ser	Asp	Cys	Ala	Ser	Leu	Pro	Ser	Ala	Leu	Gln	Ala	Gly	Cys	Lys
270					275					280					
Trp	Arg	Phe	Asn	Trp	Phe	Lys	Asn	Ser	Asp	Asn	Pro	Thr	Met	Thr	Phe
285					290					295					
Lys	Glu	Val	Thr	Cys	Pro	Ala	Glu	Leu	Thr	Thr	Arg	Ser	Gly	Cys	Glu
300					305					310					
Arg Lys															
315															

<210> 8 .

<211> 1017

<212> DNA

<213> Mucor circinelloides CP99001

<220>

<221> sig_peptide

<222> (1)... (66)

<221> mat_peptide

<222> (67)... (1017)

<400> 8

aig aag ttc acc gtt gct att act tca atc gct gtt gca ctc gct ctc 48

Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu

-20

-15

-10

agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt 96

Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys

-5

1

5

10

ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct act 144

Gly Gly ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr

15

20

25

tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc gga 192

Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly

30

35

40

tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca tct 240

Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser

45

50

55

acc aag aca tct act acc acc gcc aag gct act gct act gtc acc acc 288

Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr

60

65

70

aag aca gla acc aag aca act acc aag aca act acc aag act agc act 336

Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr

75

80

85

90

19/73

act gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag gtc	384
Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys Val	
95 100 105	
atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg gat	432
Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp	
110 115 120	
tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act ggt	480
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly	
125 130 135	
cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc aat	528
Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn	
140 145 150	
gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac aac	576
Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn	
155 160 165 170	
caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct gcc	624
Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala	
175 180 185	
tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat gaa	672
Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu	
190 195 200	
tig acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt caa	720
Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln	
205 210 215	
gtt acc aac acc ggt ggc gat tta ggc tct aac cac tit gat tig caa	768
Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln	
220 225 230	
atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa tgg	816
Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp	

Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu

21/73

-20	-15	-10
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys		
-5	1	5
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr		10
	15	20
Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys		25
	30	35
Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln		40
	45	50
Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser		55
	60	65
Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro		70
	75	80
Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr		85
	95	100
Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr		105
	110	115
Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser		120
	125	130
Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys		135
	140	145
Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp		150
	155	160
Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr		165
	175	180
Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala		185
	190	195
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn		200
	205	210
		215

22/73

Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala
 220 225 230
 Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr
 235 240 245 250
 Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val
 255 260 265
 Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
 270 275 280
 Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
 285 290 295
 Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
 300 305 310
 Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
 315 320 325 330
 Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
 335 340 345
 Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
 350 355 360
 Glu Arg Lys
 365

<210> 10

<211> 1164

<212> DNA

<213> Mucor circinelloides CP99001

<220>

<221> sig_peptide

<222> (1)... (66)

<221> mat_peptide

<222> (67)... (1164)

<400> 10

atg aag ttc acc gtt gct att act tca atc gct gtt gca ctc gct ctc	48
Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu	
-20 -15 -10	
agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt	96
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys	
-5 1 5 10	
ggg ggc att ggc tgg act ggt cct aca tgt tgt gat gct gga tgc acc	144
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr	
15 20 25	
tgt aaa gct caa aag gat aac aaa tat tat tct caa tgt att ccc aaa	192
Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys	
30 35 40	
ccc aag ggt tcc tcc tca tca tca tca tgt agt tcc gtc tat agt caa	240
Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln	
45 50 55	
tgc ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct	288
Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser	
60 65 70	
act tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc	336
Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro	
75 80 85 90	
gga tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca	384
Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr	
95 100 105	
tct acc aag aca tct act acc acc gcc aag gct act gct act gtc acc	432
Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr	

24/73

110	115	120	
acc aag aca gta acc aag aca act acc aag aca act acc aag act agc	480		
Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser			
125	130	135	
act aci gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag	528		
Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys			
140	145	150	
gtc atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg	576		
Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp			
155	160	165	170
gat tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act	624		
Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr			
175	180	185	
ggt cct gti gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc	672		
Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala			
190	195	200	
aat gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac	720		
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn			
205	210	215	
aac caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct	768		
Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala			
220	225	230	
gcc tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat	816		
Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr			
235	240	245	250
gaa ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt	864		
Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val			
255	260	265	
caa gti acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg	912		

Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
 270 275 280
 caa atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa 960
 Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
 285 290 295
 tgg ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc 1008
 Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
 300 305 310
 tct gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt 1056
 Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
 315 320 325 330
 aaa tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc 1104
 Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
 335 340 345
 ttc aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc 1152
 Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
 350 355 360
 gaa aga aag taa 1164
 Glu Arg Lys
 365

<210> 11

<211> 346

<212> PRT

<213> Phycomyces nitens CP99002

<220>

<221> sig_peptide

<222> (-19)...(-1)

<221> mat_peptide

<222> (1)... (327)

<400> 11

Met	Lys	Phe	Ser	Ile	Ile	Ala	Ser	Ala	Leu	Leu	Leu	Ala	Ala	Ser	Ser
			-15						-10					-5	
Thr	Tyr	Ala	Ala	Glu	Cys	Ser	Gln	Gly	Tyr	Gly	Gln	Cys	Gly	Gly	Lys
			1				5					10			
Met	Trp	Thr	Gly	Pro	Thr	Cys	Cys	Thr	Ser	Gly	Phe	Thr	Cys	Val	Gly
	15					20				25					
Ala	Glu	Asn	Asn	Glu	Trp	Tyr	Ser	Gln	Cys	Ile	Pro	Asn	Asp	Gln	Val
	30				35					40				45	
Gln	Gly	Asn	Pro	Lys	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Lys	Ala	Ala	Thr
				50					55					60	
Thr	Thr	Lys	Ala	Pro	Val	Thr	Thr	Thr	Lys	Ala	Thr	Thr	Thr	Thr	Thr
			65					70					75		
Thr	Lys	Ala	Pro	Val	Thr	Thr	Thr	Lys	Ala	Thr	Thr	Thr	Thr	Thr	Thr
	80						85					90			
Lys	Thr	Thr	Thr	Lys	Thr	Thr	Thr	Lys	Ala	Ala	Thr	Thr	Thr	Thr	Ser
	95					100					105				
Ser	Ser	Asn	Thr	Gly	Tyr	Ser	Pro	Ile	Ser	Gly	Gly	Phe	Ser	Gly	Asn
	110					115				120				125	
Gly	Arg	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Ala	Trp
				130				135					140		
Asp	Gly	Lys	Ala	Ser	Val	Thr	Lys	Pro	Val	Leu	Thr	Cys	Ala	Lys	Asp
		145						150					155		
Gly	Val	Ser	Arg	Leu	Gly	Ser	Asp	Val	Gln	Ser	Gly	Cys	Val	Gly	Gly
	160					165						170			
Gln	Ala	Tyr	Met	Cys	Asn	Asp	Asn	Gln	Pro	Trp	Val	Val	Asn	Asp	Asp
	175						180						185		

Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
 190 195 200 205
 Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
 210 215 220
 Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu
 225 230 235
 Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
 240 245 250
 Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
 255 260 265
 Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
 270 275 280 285
 Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn
 290 295 300
 Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
 305 310 315
 Ile Ile Ala Lys Thr Gly Cys Glu Arg Lys
 320 325

<210> 12

<211> 1041

<212> DNA

<213> *Phycomyces nitens* CP99002

<220>

<221> sig_peptide

<222> (1)... (57)

<221> mat_peptide

<222> (58)... (1041)

<400> 12

atg aag ttc tcc atc atc gct tcc gcc ctt ctc ctc gct gcc agc tcc	48
Met Lys Phe Ser Ile Ile Ala Ser Ala Leu Leu Leu Ala Ala Ser Ser	
-15 -10 -5	
act tac gct gct gaa tgc agc caa ggc tat ggc cag tgt ggt ggc aag	96
Thr Tyr Ala Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys	
1 5 10	
atg tgg act ggt ccc acc tgc tgc acc tcc ggc ttc acc tgt gta ggt	144
Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly	
15 20 25	
gcc gaa aac aac gag tgg tac tct cag tgt atc ccc aac gat caa gtc	192
Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val	
30 35 40 45	
cag ggt aac ccc aag acc acc acc acc acc acc aag gct gcc act	240
Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr	
50 55 60	
acc acc aag gct cct gtc acc acc acc aag gcc acc acc acc acc acc	288
Thr Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr	
65 70 75	
acc aag gcc cct gtc acc acc acc aag gcc act act act acc acc acc	336
Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr	
80 85 90	
aag acc acc acc aag acc acc acc acc aag gct gcc acc acc acc tcc	384
Lys Thr Thr Thr Lys Thr Thr Thr Thr Lys Ala Ala Thr Thr Thr Ser	
95 100 105	
tct tcc aac act ggc tac agc ccc att tct ggt ggc ttc tct gga aac	432
Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn	
110 115 120 125	
ggt cgc act acc cgc tac tgg gat tgc tgc aag ccc tct tgc gcc tgg	480

Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp
 130 135 140
 gac gga aag gct tct gta act aag cct gta ctc acc tgt gcc aag gat 528
 Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp
 145 150 155
 ggt gtc agc cgt ctc ggt tcc gat gtc cag agc ggt tgc gtc ggc ggc 576
 Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly
 160 165 170
 cag gcc tac atg tgc aat gac aac cag ccc tgg gtt gtc aat gac gac 624
 Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp
 175 180 185
 ctt gcc tac ggt ttc gct gct gcc agt ctc ggt agc gcc ggt gcc tct 672
 Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
 190 195 200 205
 gca ttc tgc tgc ggc tgt tac gag ctt acc ttc acc aac act gct gtc 720
 Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
 210 215 220
 gct ggc aag aag ttt gtc gtc cag gtc acc aac acc ggt gat gat ctc 768
 Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu
 225 230 235
 agc acc aac cac ttt gat ttg cag atg ccc ggc ggt ggt gtc ggc tac 816
 Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
 240 245 250
 ttc aac ggc tgc cag tcc cag tgg aac acc aac acc gat ggc tgg ggt 864
 Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
 255 260 265
 gct cgc tat ggc ggt att agc tct att tca gag tgc gac aag ctt cct 912
 Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
 270 275 280 285

```

acc cag ttg cag gct ggt tgc aag tgg aga ttc gga tgg ttc aag aac 960
Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn
                290                295                300
gct gac aac cca gag gtc acc ttc aag gct gtt act tgc cct gcc gag 1008
Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
                305                310                315
atc att gcc aag act ggt tgc gag cgc aag taa 1041
Ile Ile Ala Lys Thr Gly Cys Glu Arg Lys
                320                325

```

<210> 13

<211> 1043

<212> DNA

<213> Artificial Sequence

<220>

<221> sig_peptide

<222> (16)... (84)

<221> mat_peptide

<222> (84)... (1043)

<400> 13

```

ggatccggg acaag atg aag ttc atc act atc gcc tcc tcc gcc ctc ctt 51
                Met Lys Phe Ile Thr Ile Ala Ser Ser Ala Leu Leu
                        -20                        -15
gcc ctc gcc ctt ggc act gag atg gcc tcc gcc gct gag tgc tcc aag 99
Ala Leu Ala Leu Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys
        -10                -5                1                5
ctc tac gga cag tgc ggc gga aag aac tgg aac ggc ccc acc tgc tgc 147
Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys

```

10	15	20	
gag agc ggc tgc acc tgc aag gtc tgc aat gac tac tac agc cag tgc			195
Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys			
25	30	35	
cig ccg agc ggc tcc tgc gga aac aag tgc agc gag tgc gcc cac aag			243
Leu Pro Ser Gly Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys			
40	45	50	
aag acc acg acc gct gcc cac aag aag acc acg acc gcc gct cac aag			291
Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys			
55	60	65	
aag act acg acc gct ccc gcc aag aag acc acg acc gtc gcc aag gct			339
Lys Thr Thr Thr Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala			
70	75	80	85
tcg act ccg tcc aac tgc agc agc tgc tct tgc gga aag tac agc gct			387
Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala			
90	95	100	
gtc agc ggt ggc gct agc ggc aac ggc gtc act acc cgc tac tgg gac			435
Val Ser Gly Gly Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp			
105	110	115	
tgc tgc aag gct tgc tgc tgc tgg ccc ggc aag gct aac gtc agc tgc			483
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser			
120	125	130	
ccg gtc aag tcc tgc aac aag gac ggc gtc acc gct ctt agc gac tcc			531
Pro Val Lys Ser Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser			
135	140	145	
aac gcc cag tcc ggc tgc aac ggc ggc aac tcc tac atg tgc aac gac			579
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp			
150	155	160	165
aac cag cca tgg gct gtc aac gac aac ctt gct tac ggt ttc gct gcc			627

Asn Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala	
170 175 180	
gct gcc att agc ggc ggt ggc gag agc cgc tgg tgc tgc tcc tgc ttc	675
Ala Ala Ile Ser Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe	
185 190 195	
gag ctc acc ttc acc tcc acc agc gtt gct ggc aag aag atg gtc gtc	723
Glu Leu Thr Phe Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val	
200 205 210	
cag gtc acc aac act ggc ggt gac ctt ggc agc tgc acc ggt gcc cac	771
Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His	
215 220 225	
ttc gat ctc cag atg ccc ggc ggc ggc gtc ggc atc ttc aac gga tgc	819
Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys	
230 235 240 245	
tcg tcc cag tgg ggc gct ccc aac gac ggc tgg ggc tgc cgc tac ggc	867
Ser Ser Gln Trp Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly	
250 255 260	
ggc atc agc tcc gcc agc gac tgc tgc tcc ctc ccc agc gcc ctc cag	915
Gly Ile Ser Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln	
265 270 275	
gcc ggc tgc aag tgg cgc ttc aac tgg ttc aag aac gcc gac aac ccg	963
Ala Gly Cys Lys Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro	
280 285 290	
tcg atg acc tac aag gag gtc acc tgc ccc aag gag atc acc gct aag	1011
Ser Met Thr Tyr Lys Glu Val Thr Cys Pro Lys Glu Ile Thr Ala Lys	
295 300 305	
acc gga tgc tgc cgc aag taa acgcagg atcc	1043
Thr Gly Cys Ser Arg Lys	
310 315	

<210> 14

<211> 40

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 14

Ala Glu Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn

1

5

10

15

Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp

20

25

30

Tyr Tyr Ser Gln Cys Leu Pro Ser

35

40

<210> 15

<211> 22

<212> PRT

<213> *Mucor circinelloides* CP99001

<400> 15

Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Ser

1

5

10

15

Gly Pro Thr Cys Cys Glu

20

<210> 16

<211> 23

<212> PRT

<213> *Phycomyces nitens* CP99002

<400> 16

Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr

1 5 10 15

Gly Pro Thr Cys Cys Thr Ser

20

<210> 17

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence

<400> 17

Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa Gly Xaa

1 5 10 15

Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn

20 25 30

Xaa Xaa Tyr Xaa Gln Cys Xaa

35

<210> 18

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 18

```

Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa Gly Xaa
 1             5             10             15
Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn
          20             25             30
Xaa Xaa Tyr Xaa Gln Cys Xaa
          35

```

<210> 19

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 19

```

Cys Ser Xaa Xaa Tyr Xaa Gln Cys Gly Gly Xaa Xaa Trp Xaa Gly Pro
 1             5             10             15
Thr Cys Cys Xaa Xaa Gly Xaa Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
          20             25             30
Xaa Tyr Ser Gln Cys Xaa
          35

```

<210> 20

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 20

Cys Ser Xaa Xaa Tyr Xaa Gln Cys Gly Gly Xaa Xaa Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Xaa Xaa Gly Xaa Thr Cys Xaa Xaa Xaa Xaa Asn Xaa
20 25 30

Xaa Tyr Ser Gln Cys Xaa
35

<210> 21

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 21

Cys Ser Lys Xaa Tyr Xaa Gln Cys Gly Gly Lys Xaa Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa

20

25

30

Xaa Tyr Ser Gln Cys Xaa

35

<210> 22

<211> 36

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 22

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro

1

5

10

15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr

20

25

30

Ser Gln Cys Leu

35

<210> 23

<211> 36

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 23

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asp Trp Asn Gly Pro

1

5

10

15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr

20

25

30

Ser Gln Cys Leu

35

<210> 24

<211> 38

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 24

Cys Ser Lys Ala Tyr Tyr Gln Cys Gly Gly Lys Asn Trp Asp Gly Pro

1

5

10

15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Asp Tyr Pro Asp Asn Pro

20

25

30

Phe Tyr Ser Gln Cys Val

35

<210> 25

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 25

Cys Ser Ser Val Tyr Xaa Gln Cys Gly Gly Ile Gly Trp Xaa Gly Pro

1

5

10

15

Thr Cys Cys Xaa Xaa Gly Ser Thr Cys Xaa Ala Gln Xaa Xaa Asn Lys

20

25

30

Tyr Tyr Ser Gln Cys Xaa

35

<210> 26

<211> 38

<212> PRT

<213> Mucor circinelloides CP99001

<400> 26

Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Ser Gly Pro

1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Ala Gln Glu Gly Asn Lys

20 25 30

Tyr Tyr Ser Gln Cys Leu

35

<210> 27

<211> 38

<212> PRT

<213> Mucor circinelloides CP99001

<400> 27

Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro

1 5 10 15

Thr Cys Cys Asp Ala Gly Ser Thr Cys Lys Ala Gln Lys Asp Asn Lys

20 25 30

Tyr Tyr Ser Gln Cys Ile

35

<210> 28

<211> 38

<212> PRT

<213> *Phycomyces nitens* CP99002

<400> 28

Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr Gly Pro

1

5

10

15

Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly Ala Glu Asn Asn Glu

20

25

30

Trp Tyr Ser Gln Cys Ile

35

<210> 29

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 29

Xaa Thr Arg Tyr Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

<210> 30

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 30

Tyr Xaa Xaa Xaa Ser Gly Gly Xaa Ser Gly

1 5 10

<210> 31

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 31

Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly

1 5 10

<210> 32

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 32

Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly

1 5 10

<210> 33

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 33

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

1 5 10

<210> 34

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 34

Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly

1 5 10

<210> 35

<211> 10

<212> PRT

<213> *Mucor circinelloides* CP99001

<400> 35

Tyr Lys Val Ile Ser Gly Gly Lys Ser Gly

1 5 10

<210> 36

<211> 10

<212> PRT

<213> *Phycomyces nitens* CP99002

<400> 36

Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly

1 5 10

<210> 37

<211> 26

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 37

Ala Lys Ala Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Gly Lys

1 5 10 15

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

20 25

<210> 38

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 38

Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys

1 5 10

<210> 39

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 39

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

1 5 10

<210> 40

<211> 17

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 40

Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys

1 5 10 15

Lys

<210> 41

<211> 18

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 41

Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala

1

5

10

15

Leu Gln

<210> 42

<211> 6

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 42

Arg Phe Asn Trp Phe Lys

1

5

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 43

aaraaylgga ayggncnac

20

<210> 44

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 44

ttraaccart traancg

17

<210> 45

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 45

ttraaccart traayct

17

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 46

caatgtcttc cctctggaag cag

23

<210> 47

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 47

tgcccttagt gacagcaatg ccc

23

<210> 48

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 48

cttccctccg cactccaagc tgg

23

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 49

ccagcttggga gtcggaagg aag

23

<210> 50

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 50

tcactaaggg cagtgacacc atc

23

<210> 51

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 51

cagagggaag acatlgagag tag

23

<210> 52

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 52

acaacattat ttctlcaaac atg

23

<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 53

aaatgccgca tcaagtttta ttg

23

<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 54

ttcactttcta cctctgttgc tgg

23

<210> 55

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 55

gtaataaaact tcatagatct atglaaaaag aatg

34

<210> 56

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 56

ggatgagtal aaaagatctt atttcttga ac

32

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 57

cactttcaga agcttttatg ccac

24

<210> 58

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 58

gagctagagc cagagttaga ag

22

<210> 59

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 59

gagaactgac atcgccctta cc

22

<210> 60

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 60

acaacattat ttcttcgaat atg

23

<210> 61

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 61

tttagcagca gaggccattt cag

23

<210> 62

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 62

ttttctatcc tgatacagag atg

23

<210> 63

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 63

gcgctcataa aacgactact acc

23

<210> 64

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 64

tgcccttagt gacagcaatg tcc

23

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 65

caagaaaata agatctttaa tactcctact

30

<210> 66

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 66

aacggcaata aggcctctga atgtagc

27

<210> 67

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 67

gaaagcaatg gccagaaaac ttctgaaag

29

<210> 68

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 68

gcttcaaaact ctctagactc tagcggc

27

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 69

cggtaaggcc gacgtcagtt ctcc

24

<210> 70

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 70

tacaggagcc aacaggggag gtg

23

<210> 71

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 71

ttcacagcag gtaggtccat tcc

23

<210> 72

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 72

cctacgggtt cgccgctgct tcc

23

<210> 73

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 73

tagataccaa caccaccacc ggg

23

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 74

tgaagttcct taccattgcc tcc

23

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 75

tggtgaaacc actcgctact ggg

23

<210> 76

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 76

ttctgcctct gactgttcta acc

23

<210> 77

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 77

aatagagtta ctctatacga tag

23

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 78

caccaccaga gacagcggag tag

23

<210> 79

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 79

tgcglttgatt atcctgacaa tcc

23

<210> 80

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 80

gcggatccat gaagttcctt accatlgcc

29

<210> 81

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 81

gcggatcctt atttcttga acagccaga

29

<210> 82

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 82

giggaggiga gatcttcatt gggaac

26

<210> 83

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 83

cagcggagta cttttagaa gcag

24

<210> 84

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 84

gggagatctt gggacaagat gaagtttatt actattg

37

<210> 85

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 85

ggtaaacaa gtctgtcgg atcctgggac aagatggcca agttcttctt tac

53

<210> 86

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 86

gggggaleccl gggacaagat gaagltcaic actalcgcct cctccgcccl cctlgccctc 60
gcctctggca ctgagatggc ctccgccgcl gagtgcicca agctctacgg ccagtgcggc 120
ggaaagaact gg 132

<210> 87

<211> 136

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 87

ggccgactcg ctgcactlgl tlcgccgagga gccgcctcggc aggcactggc tglagtagtc 60
attcgagacc ttgcaggctc agccgcctc gcagcaggcg gggccgttcc agttcttcc 120
gccgcactgg ccglag 136

<210> 88

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 88

```
gggctcagat tggacggagt cgaagcccttg gcgacggtcg tggctctctt ggcgggagcg 60
glcgtagctc tcttgtagc ggcggtcgtg gtctctctgt ggcgagcggg cgtggctctc 120
ttgtgggccg actcgctcga ctgttctcc                                     150
```

<210> 89

<211> 158

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 89

```
ggaaacaagt cgagcgagtc ggcccacaag aagaccacga ccgctgcccc caagaagacc 60
acgaccgccg ctacacaaga gactacgacc gctcccgcca agaagaccac gaccgtcgcc 120
aaggcttcga ctccgtccaa ctcgagcagc tcgtcttc                                     158
```

<210> 90

<211> 160

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 90

gtccttgttg caggacttga caggcgagct gacgttagcc ttgccgggcc acgagcacga 60
 agccttcag cagtcctcag agcgggtagt gacgccgttg ccgctagcgc caccgctgac 120
 agcgcgttac ttcccgagg acgagctgct cgagttggac 160

<210> 91

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 91

agcccatggc tggltgtcgt tgcacatgta ggagttgccg ccgttcagc cggactgggc 60
 gttggagtgc ctaagagcgg tgacgccgtc ctgtttcag gacttgacag gcgagctgac 120

<210> 92

<211> 118

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 92

ggtgagctcg aagcaggagc agcaccagcg gctctcgcca ccgccctlaa tggcagcggc 60

agcgaaaccg taagcaaggt tgcgttgac agcccalggc tggltgtcgt tgcacatg 118

<210> 93

<211> 154

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 93

glgcccactt cgaatccag atgcccggcg gcggcgtcgg catcttcaac ggaigtctgt 60
cccagtgagg cgctccaac gacggctggg gctcgcgcta cggcgggaic agctccgcca 120
gcgacigtct gtccctcccc agcgccctcc aggc 154

<210> 94

<211> 154

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 94

ggggggatcc tgcgttacct tgcgcgagca tccggcttta gcggtgatct ccttggggca 60
ggtgacctcc ttgtagglica tggacgggtt gtcggcgltc tgaaccagat lgaagcgcca 120
cttgcagccg gcctggaggg cgttggggag ggac 154

<210> 95

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 95

ggggagctca ccttcaccct caccagcggt gcggcaaga agatggctgt ccaggtcacc 60
aacaciggcg gtagccttgg cagctcgacc ggigcccact tcgattccca gatgccc 117

<210> 96

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 96

ggggggatcc tgcgtttact tgcgcgagca tc 32

<210> 97

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 97

tcagcgggigg cgctagcggc aac

23

<210> 98

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 98

ctaatggcag cggcagcgaa acc

23

<210> 99

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 99

ccggtgccca cttcgatcic cag

23

<210> 100

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 100

tctttccgcc gcactgtccg tag

23

<210> 101

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 101

acgacaacca gccatgggct gtc

23

<210> 102

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 102

tcctgaatga ctactacagc cag

23

<210> 103

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 103

cccactggga cgagcatccg ttg

23

<210> 104

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 104

cgagctgctc gagttggacg gag

23

<210> 105

<211> 16

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 105

Ala Glu Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn

1

5

10

15

<210> 106

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 106

gactgaccgg tgttcaccc

19

<210> 107

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 107

ctcggttgtc atagatgigg

20

<210> 108

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 108

cccacagaag ggatccaiga lggtcgc

27

<210> 109

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 109

gcgaattcat gaagtcacc gtgtctatt

29

<210> 110

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 110

gcgaattctt actttctttc gcaacctg

28

<210> 111

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 111

cttgggtcgtg ccagcgllac cag

23

<210> 112

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 112

gcggatccat gaagttctcc atcatcg

27

<210> 113

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 113

gcggatcctt acttgcgcic gcaacca